Number of hits that pass the threshold Word size Database : OM nucleic Sequence: Perfect score: on: hed: ng table: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 2560.4 1398 1393.2 123.2 102.6 102.6 Score nucleic search, using sw model N_Geneseq_36:* Query Match 100.0 99.9 54.6 311585 seqs, 125096042 residues IDENTITY_NUC US-09-147-947-5 2562 February 27, 2000, 03:41:49; Search time 139.42 Seconds (without alignments) 4597.562 Million cell updates/sec 1 ccgacgacgcgtccgccgcc.....agatgacaacaaacggcaag 2562 GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd. . 7 8 9 9 9 9 9 9 Length 5802 1588 1588 2000 29598 28720 4360 599 DB X19027 V712589 X119027 V472590 V49654 V49654 V49654 V49657 V49668 V496766 V496766 V496766 V496766 V496766 V496766 V496776 V48878 V496796 V4 SUMMARIES .. 623170 Human SRCR protein
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EST clone DK64. Ne
EST clone DK99. N
Gp85-97 clone 18 c
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Sequence encoding DNA for human sol.
Human scavenger re
Type I macrophage
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EST clone HY435. N Sequence encoding Sequence of full-1 Mouse cytokine reg DNA sequence for m Human marcoSR cDNA Human secreted pro Human IL-1ra BAC c Gene encoding huma Protein PRO229 cDN Sequence encoding DNA for bovine sol EST clone BO358. N Human scavenger re EST clone CF118. N DNA encoding tumou Human cytokine reg Description Human marcoSR cDNA Human SRCR protein Mouse neurotrypsin Mouse serine prote-Human serine prote Human neurotrypsin 밁 õ 멅 0 B 8 B 8 B 8 멅 õ 멅 Ö 멎 421 GTCTGTAGCAGCCACTGGGATGATTCTGATGCATCAGTCATTTGTCACCAGCTGCAGCTG 480

Result No.

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	ease BSSP-3 encoding DN BSSP-3; brain tissue; s	
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	Tsuruoka N, Yamaguchi N, Yamashiro K; WPI; 99-142942/12.	
Ħ	SDB; W99087.	
Η̈́	potential ser	
ດັນ ດີ	mple 3; Page 55-60; 69pp; Japanese.	
3 8	present sequence encodes a serine procease designate isolated from human brain tissue. Transformants may be	
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RESULT 2 V72589 ID V72589 standard; cDNA to mRNA; 3350 BP. AC V72589;

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05-NOV-1998

24-APR-199D +B0625

25-SAR-1997; CH-000966

25-SAR-1997; SONDEREGGER P.
                 New human and murine neurotrypsin - used, e.g. for inhibiting tumours, treatment of neurological or lung disease, including by gene therapy and in drug development Claim 1; Page 20-24; SOpp; English.

The present sequence encodes human neurotrypsin. Neurotrypsin proteing and polynucleotides can be used: (1) to inhibit tumours, including metastases, e.g. of brain or retina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration,
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WPI; 99-009
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Human; neurotrypsin; tumour inhibition; neurological disease;
lung disease; gene therapy; drug development; stroke; brain injury;
neurodegeneration; neuroinflammatory disease; multiple sclerosis;
epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;
emphysema; bronchitis; ss.
  neuroinflammatory disease (e.g. multiple sclerosis) or
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24-JUL-1997; JP-ZI3969)
New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Example 1; Page 45-50; 69pp; Japanese.

The present sequence encodes a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs. Sequence 2614 BP; 614 A; 671 C; 799 G; 530 T;
                                                                                                                                                                                                                                                      TSURNCH OF TSURTORY LID: TSURUOKA N, Yamaguchi N, WPI; 99-142942/12.
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Mouse serine protease BSSP-3; brai
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V72590 V72590; standard; cDNA to mRNA; 2376 ВÞ

(first entry)0

Mouse neurotrypsin encoding cDNA.

Mouse; neurotrypsin; tumour inhibition; neurological disease;

Mouse; neurotrypsin; tumour inhibition; neurological disease;

Mouse; neurotrypsin; tumour inhibition; neurological disease;

Mouse; neurotrypsin; drug development; stroke; brain in

neurodegeneration; neuroinflammattory disease; multiple sclerosi

epilepsy; hypoxia; ischaemia; nerve transection; neoanglogenesi

emphysema; bronchitis; ss.

Mus musculus. Key 5'UTR Location/Qualifiers
1. .23
/*tag= a

Score 1393.2;

DB 1;

2376;

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New human and murine neurotrypsin - used, e.g. for inhibiting Lumours, treatment of neurological or lung disease, including by gene therapy and in drug development gene therapy and in drug development CC The present sequence encodes mouse neurotrypsin. Neurotrypsin proteins CC and polynuclectides can be used: (i) to inhibit tumours, including CC metastases, e.g. of brain or retina; (ii) to minimise tissue damage CC caused by stroke or brain injury (having a protective effect on the CC penumbra zone); (iii) to treat or prevent neurodegeneration, cc increase survival of damaged neurons (e.g. in cases of hypoxia, cc ischaemia, nerve transection) and to stimulate regeneration and/or restoration or synapses; (v) to treat or prevent retinal disorders (e.g. degeneration or neoangiogenesis); (vi) to prevent apoptosis (or other causes of cell death) in the nervous system; (vii) to regenerate brain cc and/or nervous tissue; (viii) to treat pain; (ix) to improve brain encous insulater consumers (x) to treat or prevent apoptosis (or other candor nervous tissue; (viii) to treat pain; (ix) to improve brain cc wide range of psychiatric disorders; and (xi) to treat or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consumers (consumers) and (xi) to treat brain or lung consum
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                                TGTCAAACAAGACATTGGAAGGCACAACTGCCGCCACAGTGAGGATGCAGGAGTCATCTG
                                            tatcaagcaagatattggaagacacaactgccgccacagtgaagatgcaggagttatttg
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Scavenger receptor cysteine rich domain; SRCR; diagnosis; tr
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                                                          Location/Qualifiers 107. .5464
                                    /product= SRCR protein"
                                               /*tag=
           "Scavenger receptor cysteine-rich containing protein"
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Best Local Similarity
Matches 522; Conserv
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09-JAN-1998; D00096.
18-JUL-1997; DE-030997.
09-JAN-1997; DE-000519.
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
MOLLenhauer J, Poustka A;
WPI; 98-399136/34.
P-PSDB; W64591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteins containing scavenger receptor, cysteine rich domain useful for diagnosis and treatment of tumours Claim 4; Fig 2; 54pp; German.

This sequence encodes a human protein which contains a SRCR (scavenger receptor, cysteine-rich) domain. The gene and encoded protein can be used to diagnose or treat tumours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist and to assess the significance of individual forms on cellular properties. The protein can be used to detect the presence of autoantibodies and antibodies which regulate its expression.

Sequence: 5802 BP; 1253 A; 1614 C; 1576 G; 1359 T;
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                   caggcgacagtggggaaggcatgactgcagccaccgcgaagatgttagcattgcctgcta 1298
                                                                                                                                     GCTGGGCTGTGGGCCACGTCAGCCCCCAGGAAATGCCCCGGTTTGGCCCAGGGTTCAGG
                                                                                                                                                                      gttgggatttaaatatggtaaacaagcatctgccaa---ccattttgaagaaagcacagg 1178
                                                                                                                                                                                                          CTGGGGCACCGTGTGTGATGACTACTGGGACACCAATGATGCCAATGTGGTTTGCAGGCA
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CCACAATGGCTGGCTCTCCCACAACTGTGGCCATCATGAAGACGCTGGTGTCATCTGCTC
                                                                  ACCCATTGTCCTGGATGATGTGCGCTGCTCAGGACATGAGTCCTATCTGTGGAGCTGCCC
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Sequence
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ecceptor protein, and fragments and analogues thereof may be ecceptor protein, and fragments and analogues thereof may be important used in assay and purification of the albit target. Labelled Abs, raised to the protein may be injected into the vascular system to detect the presence of atherosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1990 (first entry)
Sequence encoding portion of scavenger receptor protein with
seffinity for acylated low density lipoprotein (aLDL).
Acylated low density lipoprotein; aLDL; atherosclerotic plaque;
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                                                                                                                                                                                                                                                                                                                                                     New receptor protein - has affinity for acetylated low density lipoprotein corresponding antibodies and DNA sequences.
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WPI; 90-193408/25.
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                                                                                        agtggggaaccgtttgtgatgaccaatgggatgatgccgatgcagaagtgatctgcaggc 799
                                                                                                                      TCCGACTGGTGGGTGGCAGCGGCCCTCACGAAGGCAGAGTGGAGATTTTTCACGAAGGCC 1117
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Pred. No. 1.4e-15;
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                                                                                                                                                                                                                                                                                                                                                                    portion of a macrophage scavenger receptor protein

The bovine scavanger receptor protein gene was isolated by screening

The bovine scavanger receptor protein gene was isolated by screening

The bovine scavanger receptor protein gene was isolated by screening

a bovine lung cDNA library with degenerate probes designed based on

fragments of the purified scavanger receptor protein. The DNA encodes

a scavanger receptor protein which has a binding capacity for

acetylated low density lipoprotein (LDL) and binds endotoxin.

Fragments of the extracellular portion of the scavanger receptor

protein inactivate endotoxin-related substances and are used in the

diagnosis and treatment of endotoxaenia. They may be administered

tragments may also be fixed to inert supports for purificn. purposes.

The fragments may be modified to have greater binding affinity for

the endotoxin-related substance than the native scavanger receptor

protein, or to more effectively neutralise the toxic or pathogenic

effects of mols. that bind the scavanger receptor protein or of

organisms which express such mols.

See also Q28536-9.

304 C; 367 G; 411 T;
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Best Local Similarity
Matches 177; Conserv
                                                                                                                                     1118
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Q28540;
16-FEB-1993 (first entry)
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Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-1993 (first entry)
DNA for bovine sol. scavanger receptor.
Macrophage; endotoxaemia; radiolabelled; toxic; degenerate;
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22-FEB-1991;
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Pred. No. 1.4e-15;
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Number of hits that pass the threshold : 428588

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6D_COMB.seq:*
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       Length
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 PCT-US95-04467-6
US-08-458-568A-1
US-07-957-039A-7
US-08-153-799-17
S188829-2
US-08-200-900A-1
US-08-681-151-2
PCT-US94-00616-1
US-08-254-922-1
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US-08-473-791-9
US-08-433-117-14-9
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US-08-948-222-1
US-08-973-145-1
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ctctaco atttte gaagtg gaagtg tttgggto tttggaa tttggaa tcaattg tccattg tccattg tccattgaa gctggag	Length	ANTIRODY	טי טי
ctaccatgctggcc 	in the second se	ODV 4	Sequence
cgctggcc 	8 8		
;c 739; c 11117; c 199; a 1177; g 859; g 1237; c 919; a 1297; a 1297; a 1297; a 1357; a 1357	Gaps		180, App 180, App 180, App 1, Appli 1,
9 9 9 9 9 9 9 9 9 9 9	0	17 17 1	0, App 0, App 0, Appli Appl
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RESULT 2 US-08-470-350B-1 ; Sequence 1, Application US/08470350B ; Patent No. 5684126

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Watches
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TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Li, Xiao
APPLICANT: Snyder, Solomon H
TITLE OF INVENTION: Ebnerin: A Secreted von Ebner's Gland
TITLE OF INVENTION: Protein Associated with Taste Buds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
1258 GTCATCTGT 1266
                                1630
                                                                1198
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                                                                                                                              1138 CAAGGCTCTGGATCCATTGTTCTGGATGACGTGGCCTGTACAGGACATGAGGCCTATCTG
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                                                                                                                                                                                                                                                              1018 TACCAGGGTTCCTGGGGTACCGTGTGTGACGACAGCTGGGGACACCAAGGATGCCAACGTG
                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 4360 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Wolffe, Susan A
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
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                                                                                                                                                                                                                                                                                                                            958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULL NOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Paice-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity les 177; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                gaaggaaaaggacccatccatgtggataatgtgaagtgcacaggaaatgagaggtccttg 1569
                                                                                  gctgactgtatcaagcaagatattggaagacacaactgccgccacagtgaagatgcagga 1629
                                                                                                                                                                                                                       atctgtcgtcagcttggctacaagggtcctgccagagcaagaaccatggcttacttttgga 1509
                                                                                                                                                                                                                                                                                                                           GGTTTGGCTGTGAGGCTGGAATGGAGGAGACAGGTGTCAGGGTCGTGTGGAGATCCTT 1017
                                gttatttgt 1638
                                                                TGGAGCTGCTCCCACCGAGGCTGGCTCTCTCATAACTGTGGCCACCATGAGGATGCTGGA 1257
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1001 G Street, N.W.
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Pred. No. 4
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MOLECULE TYPE:

US-08-477-674-9
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                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Koths,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 420-3152
TELEFAX: (510) 658-5470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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 428
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/OFILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman, Kenneth M.
REGISTRATION NUMBER: 34,174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                        gcagctgggcctcagtggcattgccaaagcatggcatcaggcatattttggggaagggtc 857
                           tggcccagttatgttggatgaagtacgctgcactgggaatgagctttcaattgagcagtg 917
                                                                                                                                AGGCCCCATCATGCTGGACGAGGTCCAGTGCACGGGAACCGAGGCCTCACTGGCCGACTG
                                                                GGCCCTGGGCTTCGAGAACGCCACCCAGGCTCTGGGCAGAGCTGCCTTCGGGCAAGGATC
                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                                               Score 94.4; DB 1;
Pred. No. 2.7e-16;
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                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                              Length 2285;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-473-791-9
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US-08-473-791-9
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                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2285 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             NAME: Goldman, Kenneth M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 2595.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 420-3152
TELEFAX: (510) 658-5470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
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                                  308
                                                                                                               678 cattcgccttgctggaggcagcagtgtgcatgaaggccgggtggagctctaccatgctgg 737
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798 gcagctgggcctcagtggcattgccaaagcatggcatcaggcatattttggggaagggtc 857
                                                                                            248 CATGCGGCTGGCCGATGGGGGCGCCCACCAACCAGGGCCGCGTGGAGATCTTCTACAGAGG 307
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                  Similarity
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1400 Fifty-Third Street
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                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taylor, Eric
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                                                                                                                                                                       3.7%;
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                                                                                                                                                       Score 94.4; DB 2;
Pred. No. 2.7e-16;
0; Mismatches 136;
                                                                                                                                                          136;
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US-08-316-714-9
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US-08-316-714-9
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                                                                Matches
                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2285 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 25:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 420-3152
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth M
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/961,404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,714
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MEDIUM TYPE: Floppy disk
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               678 cattcgccttgctggaggcagtgtgcatgaaggccgggtggagctctaccatgctgg 737
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                                                                                                                                                                                                                                                                                          (510) 658-5470
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Halenbeck, Robert F.
                                                                Conservative
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                                                            Score 94.4; DB 4;
Pred. No. 2.7e-16;
0; Mismatches 136
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LENGTH: 2037 base pairs
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MEDIUM TYPE: Floppy disk
                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
LIBRARY: THP-1
PUBLICATION INFORMATION:
AUTHORS: Ashkenas, et
JOURNAL: J. Lipid Res.
                                                                                                                                                 MOLECULE TYPE:
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6392
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                                                                                                                   ANTI-SENSE:
                                                                                                                                YPOTHETICAL:
                                                                  MMEDIATE SOURCE:
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ITLE OF INVENTION: Method for Treating Gram-Positive
ITLE OF INVENTION: Septicemia
                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
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                                                                                  ORGANISM:
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(404)-815-6555
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US-08-453-117-1
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Best Local Similarity
Matches 176; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                   INFORMATION FOR SEQ
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,
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                                                                                                    REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLICANT: Brawner, Mary E.
TILE OF INVENTION: Attachment Enhanced
                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      ZIP: 19406-5090
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DATE: 1993
                                                                                    TELEPHONE:
                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                SOFTWARE:
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: 2028 base pairs nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                         Pennsylvania
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                                                                     (610)
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                                                                                      (610) 270-5019
                                                                     270-5090
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Pred. No. 3.7e-16;
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Page 5
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; STRANDEDNESS: double
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US-08-453-117-1
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Search completed: February 27, 2000, 21:33:35 Job time: 177 sec
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1383 GAGTCACTTGCAC 1395
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Title: Perfect score: Sequence:

Word size Database :

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em_est16:* em_est17:* em_est18:*

em_est19

gb_est8:* gb_est6:*
gb_est7:* gb_est3:*
gb_est4:* gb_est1:*
gb_est2:*

gb_est5:*

em_est12:*
em_est13:*
em_est14:*

em_est11:* em_est10:*

em_est15:*

em_est7:* em_est6:* em_est5:* em_est2:* em_est1:*

em_est4:* em_est3:*

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Number of hits that pass the threshold
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AI968581
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AW104566
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AI958581 wt90c08.x
AI457628 tj63e07.x
AA460641 zx6zd12.r
AW188298 xj94h04.x
AW104566 xd78h09.x
AA928660 om75908.s
AA166524 ms46a12.r
                                                                 Description
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On Jun 22, 1998 this sequence version replaced g1:3246664. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	wt90008.x1 NCI_CGAP_GC6 HIMMO Sapiens cDNA clone IMAGE:.5514734 3' similar to TR:008762 008762 PROTEASE, SERINE, 12 NEUROTRYPSIN, ;, mRNA sequence. A1968581 A A1968581 GI:5765399 SEST. Homo sapiens EUKARYOTA; Metazoa: Chordata; Craniata; Vertebrata; Mammalia; EUKARYOTA; Metazoa: Chordata; Craniata; Vertebrata; Mammalia; EUKARYOTA; Metazoa: Catarrhini; Hominidae; Homo. (CE () Lases 1 to 684) NRS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NALIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)	4 3.7 \$40 49 AL047474 4 3.7 \$411 46 AI449832 8 3.7 \$411 51 AI734941 8 3.6 474 35 AA581208 2 3.6 455 50 AI677867 3 3.5 382 28 281180 6 3.5 382 28 281180 6 3.5 616 45 AI341167 2 3.4 468 46 AI415453 ALIGNMENTS	317 12.4 440 4 AII5 314 12.3 413 44 AI32 314 12.3 483 44 AI32 314 11.6 448 63 AI65 6.4 11.6 448 63 AI65 6.4 11.6 448 63 AI65 7.4 11.6 448 63 AI65 7.1 10.6 274 32 AA37 271 10.6 274 32 AA37 3.4 91 379 62 AI89 3.4 91 379 62 AI89 3.2 8.7 303 43 AI32 3.2 8.7 303 70 AV25 3.4 4.9 230 70 AV25 3.4 6 123 37 AA68 3.8 4.6 126 70 AV26 6.6 4.4 4.5 424 74 AW20 6.6 4.4 4.5 424 74 AW20 6.6 4.4 4.5 424 74 AW189 6.6 4.2 446 74 AW189 6.6 4.3 3.9 705 81 BI63 6.6 3.9 705 81 BI63 6.6 3.8 570 79 GGA11	.2 12.8 622 60 AI808920
Qy 2402 attotcotggtgtttataccaaagtctcagcctttgtaccttggataaaaagtgtcacca 2461	Qy 2102 9d03d9CCCACCAGAGACCCCCCCCCCCCCCCCCCCCCCCCCCC	1924 tatcatactctggtaccagaggagtttgaggaagaaattggagttcaacagattgtgatt	High quality sequence stop: 410. Location/Qualifiers 1684 //db_xref="Homo sapiens" //dlone="INAGE:2514734" //clone="INAGE:2514734" //clone="INAGE:2514734" //clone="INAGE:2514734" //clone="INAGE:2514734" //clone="INAGE:2514734" //clone="INAGE:2514734" //clone="INAGE:2514734" //lab_host="pooled germ cell tumors" //lab_host="pooled germ cell tumors" //lab_host="pliDB" //note="Yector: p773D-Pac (Pharmacia) with a modif polylinker; plasmid DNA from the normalized librar NCI_CGAP_GC4 was prepared, and ss circles were made vitro. Following HAP purification, this DNA was us tracer in a subtractive hybridization reaction. The was PCR-amplified cDNAs from a pool of 5,000 clone from the same library (cloneIDs 1257095-1258631, 1469064-1470983, and 147592-1476743). Subtraction Bento Soares and M. Fatima Bonaldo. " 164 a 175 c. 141 g 204 t atch 23.5%; Score 602.6; DB 63; Length 684; cal Similarity 98.3%; Pred. No. 4.2e-134; Gasconservative 0; Mismatches 9; Indels 2; Gasconservative 0; Mismatches 10	www-bio.llnl.gov/bbrp/image/image.html

REFERENCE AUTHORS TITLE

TRGANISM SDS

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CCCAGAAAACAGCATCCANCTGTTACATACCAGGATGGGGTGACACAGGCCGAGCCTATT 554
                                                                                                 ataagggtcggtttacagggagaatgctttgtgctggaaacctccatgaacacaaaacgcg 2293
                                                                                                                                                                                              caagaacactacaacaagcagccattcccttacttcctaaaaggttttgtgaagaacgtt 2233
                                                                                                                                                                  CAAGAACACTACAACCAGCCATTCCCTTACTTCNTAAAAGGTTTTGTGAAGAACGTT 494
                                                                      ATAAGGGTCGGTTCACAGGGAGAATGCTTTGTGCTGGAAACCTCCATGAACACAAACGGG 434
                                                                                                                                                                                                                                                                                                                                                                 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997) on May 18, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 113 Std Error: 0.00 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1457628 614 bp mRNA EST 13-APR-1999 tj63e07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2146212 3' similar to TR:008762 008762 NEUROTRYPSIN
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 614)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              Conservative
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138 c 124 g 204 t
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/lab_host="DH10B"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                  16.4%;
95.8%;
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Pred. No. 2.6e
0; Mismatches
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On Sep 12, 1996 this
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA460641 397 bp mRNA

EST 09-JUN-1997

ZX62d12:r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone

IMAGE:796055 5' similar to SW:TRY2_CANFA P06872 TRYPSINOZEN,

ANIONIC PRECURSOR ; contains Alu repetitive element; mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 397)
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                  115
            and Eco RI sites of the modified pT7T3 vector. Librwent through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                              Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I
                                                                                                                                                                                                                                 /clone_lib="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                  /clone="IMAGE:796055"
                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:6039851"
/db_xref="taxon:9606"
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REFERENCE
AUTHORS
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396; Conserv
                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40Up from Gibco
High quality sequence stop: 475.
Location/Qualifiers
                                                                                                                                                                                                                                                                                             Unpublished (1997)
on Apr 30, 1999 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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AW188298.1 GI:6462734
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/note-*Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBL) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver
                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2664919"
/clone=lib="Soares_NFL_T_GBC_S1"
                                                                                                              /lab_host="DH10B"
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Pred. No. 1.1e-84;
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AUTHORS
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AW104566/c
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Best Local Similarity
Matches 395; Conserv
                                                     source
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                                                                                                                Tel: (301) 496-1550
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty free through LLNL; contact the
                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 537)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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AW104566 ESTATEMENT OF TR:008762 008762 NEUROTRYPSIN, ; mRNA sequence.
                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
On Mar 10, 1998 this sequence version
Contact: Robert Strausberg, Ph.D.
                                                                                      IMAGE Consortium (info@image.llnl Seq primer: -40UP from Gibco High quality sequence stop: 315.
                                                                                                                                                                                                                                                                                                                                                                            human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " Fatima Bonaldo."
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2603777"
                                                                    Location/Qualifiers
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95.4%;
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Pred. No. 1.3e-81;
0; Mismatches 19
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2 PROTEASE,
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KEYWORDS
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                                                                                                                    TITLE
                                                                                                                                      AUTHORS
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Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2045775.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                        sequence.
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om75g08.s1 NCI_CGAP_GC4 Homo
similar to TR:008762 008762 N
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 478)
                                                                                                                                                                                                                Homo sapiens
                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                      EST
                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                        AA928660.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and s circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 728906-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                          GI:3076951
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O Sapiens CDNA Clone IMAGE:1553054
NEUROTRYPSIN PRECURSOR. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337; DB 69;
No. 1.7e-70;
                                                                                                                  Genome Anatomy
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                                                                                                                  Project (CGAP),
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Best Local S
Matches 346
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                                                                                                                                                                                                                                                                                                                tttgaacccccactattagcactcagcagagatgacaacaaacggcaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTCAAGGATTCTCCTGGTGTTTATACCAAAGTCTCAGCCTTTGTACCTTGGATAAAAAG
                                                                                                        AA166524 470 bp mRNA EST 19-DEC-1996 ms46a12.rl Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cDNA clone IMAGE:614590 5', similar to SW:URCT_MOUSE P11214 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR;, mRNA sequence.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata;
                                                                             AA166524.1
                                                                                                 AA166524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Christopher A. Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 616 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality seguence stop: 382.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled germ
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1553054"
/clone_lib="NCI_CGAP_GC4"
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Pred. No. 9.7e-70;
0; Mismatches 2;
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Mammalia;

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agagagagg 2112
|||||||||
                                                                CCAGGGGAGCAATGTGCCAGACTAAGCACCCACGTTTTGCCAGCCTGTTTACCTCTATGG 461
                                                                                                                                                                         tatcatactctggtaccagaggagtttgaggaagaattggagttcaacagattgtgatt 1983
                                                                                                                                                                                                                                                                                                                                                                                                                         ggagatggcaggctcctctgcggggctacgctcctgagtagctgctgggtcctcacagca 1863
                                                                                                                                                 CACAGGAACTACAGGCCAGACAGAAGCGACTATGACATTGCCCTGGTTAGATTGCAAGGA
                                                                                                                                                                                                                                   TATCATACTCTGGTACCAGAGGAGTTTGAACAAGAAATAGGGGTTCAACAGATTGTGATT 341
                                                                                                                                                                                                                                                                                                                GCACACTGCTTCAAAAGGTACGGAAACAACTCGAGGAGCTATGCAGTTCGAGTTGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                  GGAGACGGCAGGCTGCTTTGTGGAGCTACCCTTCTGAGTAGCTGCTGGGTCCTGACAGCT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 470)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1404667.
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 86.(
69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:375414
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h quality sequence stop: 439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-Torgan: whole embryo; Vector: pCMV-SPORT2; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. 13.5dpc embryos. pCMV-SPORT2 vector."

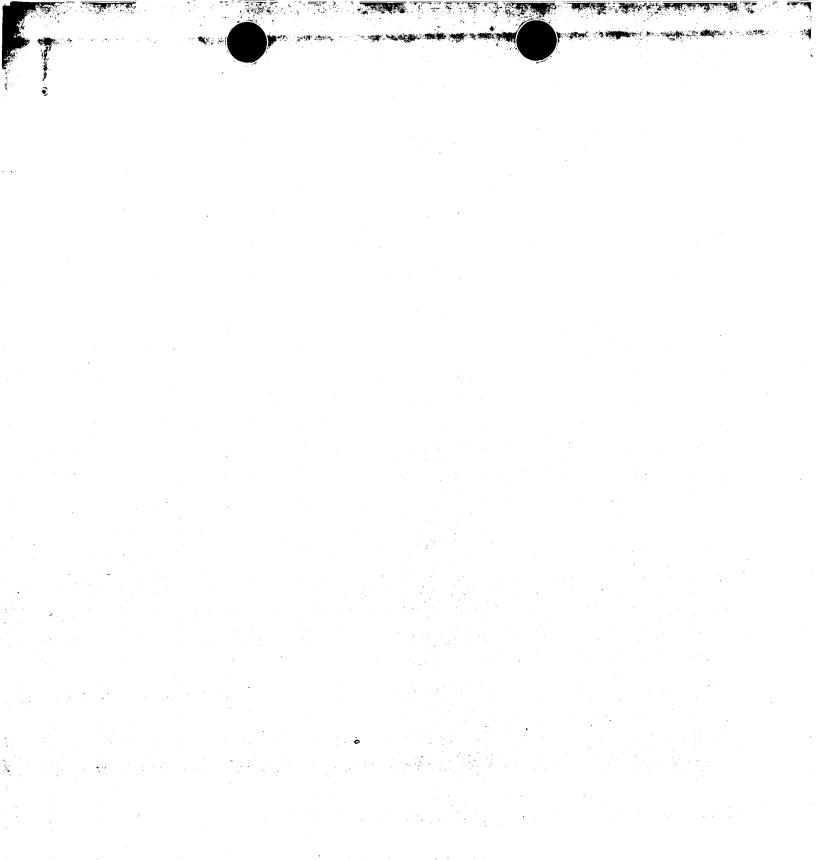
a 106 c 135 g 113 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="Taxon:10090"
/clone="IMAGE:614590"
/clone=lib="Life Tech mouse embryo 13 5dpc 10666014"
/tissue_type="embryo"
/dev_stage="13.5dpc embryos"
/lab_host="9H10B"
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Pred. No. 1.5e-69;
0; Mismatches 60;
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Db 462 AGAGAGAGG 470

Search completed: March 2, 2000, 21:56:44 Job time: 6493 sec



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Mon Mar 13 10:00:13 2000: Margan +imo 10 00 conside	protein - protein database search, using Smith-Waterman algorithm	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	***************************************	**************************************

on: Mon Mar 13 10:09:43 2000; MasPar time 18.99 Seconds 560.722 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-09-147-947-6 (1-822) from US09147947A.pep (1 of 2) 6328

Sequence: 1 PTTRPPPPLPRFPRPPRALP......PGVYTKVSAFVPWIKSVTKL 822

Scoring table: PAM 150 Gap 11

Searched: 131253 seqs, 12956647 residues

Past-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued

1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 35.408; Variance 155.210; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,	Score	Match	Length	BB	ID	Description	Pred. No.
_	0		ω	2		Sequence 3, Applicatio	5.78e-44
N	S		S	N	-08-68	equence 1, Applicati	.12e-4
ω	583	9.2	355	N	-08-81	ce 47, Āpplicat	-4
4	ന		ω	_	7-9	equence 3, Applicat	.35e-4
رن ن	ന		ω	N	8-81	equence 51, Applica	.37e-
თ	ന		ν	N	8-8	equence 39, Applicat	.37e-
7	~		Ç	Н	-08-42	e 6, Applic	. 7
œ	-	9.1	5	4	256-	atent No. 522325	.79e-
9	7		5	ᆫ	-08-4	quence 2, A	.79e-
10	7	9.1	S	Н	US-08-217-	equence 1, Applicat	.79e-4
11	~ 1	•	ū	ب	-08 - 13	ce 1, Applicat	.79e-4
12	V		ū	Ц	US-08-217-	equence 1, Applicat	.79e-
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15	V		G	ш	-08-4	equence 8, Applicati	.04e-4
16	~1		5	Н	-08-42	e 4, App	.79e-4
17	V		σ	۲	8-72	equence 83, Ap	٠
18	~1		σ	_	8-09	equence 83, Applicat	.29e-4
19	V		9	N	g	се 44, Ар	.29e-4
20	~	9.1	\vdash	_	-08-1	equence 18, Applicat	.29e-
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411	527	437	430	389	383	355	331	306	562	562	562	562	562	562	562	527	527	527	472	437	432
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● US-08-560-	5520913-1	US-08-811-	569	8-80-	US-08-558-	US-08-811-	US-08-560-	US-08-560-	-80	US-08-560-	5244676-5	340	5185259-3	3-8	773	1	US-07-609-	5185259-8	8-80-	US-08-811-	US-08-560-
ce 48,		57,	0.5	65,	0 6,	OD UT	e 46,	e 45,	38,	Sequence 50, Applicati		Patent No. 5200340.	Patent No. 5185259.	Sequence 43, Applicati		2, 1	Sequence 16, Applicati	Patent No. 5185259.	e 63	uence 49, Ap	Sequence 47, Applicati
.13e-	1.11e-40	7.24e-41	4.70e-41	4.70e-41	7.24e-41	.11e-	4.70e-41	4.70e-41	.79e-	. 7	.79e-4	.79e-	3.79e-41	.79e-	.79e-	.79e-	3.79e-41	3.79e-41	. 7	. 7	1.29e-41

ALIGNMENTS

COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: US/08/681
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive TELEFAX: STREET: 3174 POI CITY: Palo Alto STATE: CA 415-845-4166 US/08/681,151 PF-0074US

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08681151
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                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08681151 Patent No. 5869637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            812 FVPWI 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   617 YIDWI 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  448 YGG-ILNL-SEITNK-TPFSSIKELIIHQKYKMSEGSYDIALIKLQTPLN-YTEF--QK- 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          752 RMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 YAVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVL 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity nes 96; Conserv
                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                         APPLICANT:
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LIBRARY: GENEA
CLONE: 205011
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QMICAGY-KEGG-IDACKGDSGGPLVCKHSG-RWQLVGITSWGEGCARKEQPGVYTKVAE 616
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                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
                                                                                                         SOFTWARE:
                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                      STREET:
                    FILING DATE
                                                                                                                                                                                                                                  ADDRESSEE:
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JE OF INVENTION: A NOVEL HUMAN KALLIKREIN
SER OF SEQUENCES: 4
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llarity 39.2%;
Conservative
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Bandman, Olga
Braxton, Scott Michael
                                                                                                       FastSEQ Version 1.5
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linear
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                                                                                                                              IBM Compatible
                                                                                                                                           Diskette
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                                                                                                                     DOS
                                                                              US/08/681,151
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Pred. No. 5.78e-44;
60; Mismatches 71
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Best Local Similarity 40.9%;
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 CGXRPAARMNKRILGGRTSRPGRWPWQCSLQ--SEPS-GHI-CGCVLIAKKWVLTVAHCE 159
                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 DMKTITTRMICAG--YESGTVDSCMGDSGGPLVCEKPGGRWTLFGLTSWGSVCFSKVLGP 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 KRYGNSTRSYAVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQ 685
                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: HEARN
CLONE: 307474
                                                                                       APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
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       COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                               KGR-FTGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKD-SP 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARFSSHVLPACLPLWRERPQKTASNCYITGWGDTGRAYSRTLQQAAIPLLPKRFCEERY 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SE--TGYVRPVCLPN-PEQWLEPDTYCYITGWGHMGNKMPFKLQEGEVRIISLEHCQSYF 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGRENAA-VXKVVLGINNLDHPSVFMQTRFVKTIILHPRYSRAVVDYDISIVEL--SEDI 216
                                 CITY: ARLINGTON STATE: VA
                                                      ADDRESSEE: P.C. STREET: 1755 S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 AA; 39995 MW; 717455 CN;
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                                                                                                                                                                    NIWA, MINEO
SAITO, YOSHIMASA
SASAKI, HITOSHI
                      USA
                                                                                                                                             HAYASHI, MASAKO
NOTANI, JOUJI
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                                                                                 OBLON,
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                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                          JEFFERSON
                                                                                  SPIVAK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 597; DB 2;
Pred. No. 2.12e-43;
43; Mismatches 93
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                                                                                  MCCLELLAND, MAJER & NEUSTADT
                                                          DAVIS
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                          HIGHWAY,
                                                                                                                                                                                                                                                                                                                                  355
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                                                                                                                                                 Sequence 3, Application US/07942157A Patent No. 5648253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              644 TLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRE 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 IGRHN-CRHSE-DAGVICDYF-GKKAS-GNSNKESLSSVCGLRLLHRRQKRIIGGKNSLR 586
                                                                                                                                                                                                                                                                                                                                                                                                                         289 TRSGGPQANLHDACQGDSGGPLVCLNDGRMTLV-GIISWGLGCGQKDVPGVYTKVTNYLD 347
                                                                                                                      GENERAL INFORMATION: APPLICANT: Wei, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 LGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPS-CSTCGLRQYSQPQFRIIGGLFADI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 9.2%;
Local Similarity 37.6%;
les 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 47:
STREET: 11.
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                       APPLICANT: Wei, Cha-Mer TITLE OF INVENTION: Inh:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein IENCE 355 AA; 39543 MW; 638851 CN;
                                                                             NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPP-AD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWPWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHCFK-RYGNSTRSYAVRVG-DYH 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPOKTASNCYITGWG--DT-GRAYSRTLQQAAIPLLPKRFC-EERYKGR-FTGRMLCAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERF--PPHHLTVILGRTYR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGD 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                   1100 Peachtree Street Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                 Kilpatrick & Cody
                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                       Inhibitor-Resistant Urokinase
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Pred. No. 4.37e-42;
66; Mismatches 101;
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                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                               430
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Best Local
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          Sequence
                                                                  XXXXXX
                                                                                            US-08-811-949-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               153 GKKPSSPPE-E-LKFQCGQKTLRPRFK-IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCG
                                                                                                                                                                              385
                                                                                                                                                                                                                                                                670
                                                                                                                                                                                                                                                                                                                     610 ATLLSSCWVLTAAHCFKRYGNSTRSYAVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR 669
                                                                                                                                                  782
                                                                                                                                                                                                                                   327 YPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAAD-PQWK-TDSCQGDSGGPLVCSLQ 384
                                                                                                                                                                                                                                                                                           269 LAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYND-PQ-FGTSCEITGFGKENSTDYL 326
                                                                                                                                                                                                                                                                                                                                                 210 GSLMSPCWVISATHCFIDYPKKE-DYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADT 268
                                                                                                                                                                                                                                                                                                                                                                               550 GKKASGNSNKESLSSVCGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCG 609
                                                                                                                                                                                                                                                                                                                                                                                                                            9.2%;
Local Similarity 37.1%;
les 104; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,157A
FILING DATE: 19920908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/631673
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                  GRM-TLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTK 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide LOCATION: 1..19 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
LOCARTON: 198..203
COTHER INFORMATION: /label= modified
OTHER INFORMATION: /note= "six amino acids deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYPOTHETICAL:
                                                                                                                                                                                                                                                               -SDY-DIALVRLQGPEEQCARESSHVLPACLP-LWRERPQKTASNCYITGWG-DTGRAY- 724
                                                                                                                                                                                                          -SRTLQQAAIPLLPKRFCEE-RYKGR-FTGRMLCAGNLHEHKRVDSCQGDSGGPLMCERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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           51,
          Application US/08811949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 amino acids
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                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= peptide
/note= "WAP signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 580; DB 1;
Pred. No. 8.35e-42;
66; Mismatches 93
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Best Local
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GENERAL IN
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                                                                                                                                                                                                                                                                                                                                              Match 9.2%;
Local Similarity 37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION UMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPBAN: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein 965246 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
                           WIR 432
                                                      LHE---HKRV-DSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVP 814
                                                                                TRSGGPQANLHDACQGDSGGPLVCLNDGRMTLV-GIISWGLGCGQKDVPGVYTKVTNYLD 429
                                                                                                                                    LQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGD 370
                                                                                                                                                                TLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRE 703
                                                                                                                                                                                                                      GGWPWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHCFK-RYGNSTRSYAVRVG-DYH
                                                                                                                                                                                                                                                                             IGRHN-CRHSE-DAGVICDYF-GKKAS-GNSNKESLSSVCGLRLLHRRQKRIIGGKNSLR 586
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                                                                                                          RPOKTASNCYITGWG--DT-GRAYSRTLQQAAIPLLPKRFC-EERYKGR-FTGRMLCAGN
                                                                                                                                                                                -VVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPP-AD 310
                                                                                                                                                                                                                                                  ASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERF--PPHHLTVILGRTYR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLOW, GEARM.
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                    114;
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5840533
                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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HAYASHI, MASAKO
NOTANI, JOUJI
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                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acids
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Pred. No. 4.37e-42;
66; Mismatches 101;
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                                                                                                                                                                                                                                                                                                                                                             Length 437
                                                                                                                                                                                                                                                                                                                                   Indels
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Best Local S
Matches 11
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MOLECULE TYPE: protein
SEQUENCE 527 AA; 59027 MW; 1397140 CN:
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461 TRSGGPQANLHDACQGDSGGPLVCLNDGRMTLV-GIISWGLGCGQKDVPGVYTKVTNYLD : : |:||||||||||: ::
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                                                                                                                                                                                               531 IGRHN-CRHSE-DAGVICDYF-GKKAS-GNSNKESLSSVCGLRLLHRRQKRIIGGKNSLR 586
                                                                                                                                                                                                                         226 LGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPS-CSTCGLRQYSQPQFRIIGGLFADI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39,
                                                                                                                                                                                                                                                 Match 9.2%;
Local Similarity 37.6%;
les 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
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                                                                                          TLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRE
                                                                                                                                              GGWPWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHCFK-RYGNSTRSYAVRVG-DYH
                                                                                                                                                                     ASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERF -- PPHHLTVILGRTYR 342
                                                                                                                  -VVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPP-AD
                                      RPQKTASNCYITGWG--DT-GHAYSRTLQQAAIPLLPKRFC-EERYKGR-FTGRMLCAGN
                                                                LQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGD
                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUS ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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NOTANI, JOUJI
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                                                                                                                                                                                                                                                 Score 583; DB 2; Le
Pred. No. 4.37e-42;
66; Mismatches 101;
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                                                                                                                                                                                                                                                                           Length 527;
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         759
                             289 TRSGGPQANLHDACQGDSGGPLVCLNDGRWTLV-GIISWGLGCGQKDVPGVYTKVTNYLD 347
                                                                                                                                                                                             229
                                                                                                                                                                                                                                                                                            171 -VVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPP-AD 228
                                                                                                                                                                                                                                                                                                                                                                                       587
                                                                                                                                                                                                                                                                                                                                                                                                                     531 IGRHN-CRHSE-DAGVICDYF-GKKAS-GNSNKESLSSVCGLRLLHRRQKRIIGGKNSLR 586
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                                                                                                                                  704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       815 WIK 817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATE:
FILING DATE:
CLASSIFICATION: 435
CRISCATION DATA:
APPLICATION NUMBER: 07/689,410
APPLICATION NUMBER: 1991
TIME DATE: 22 APRIL 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                759 LHE---HKRV-DSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVP 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22 APRIL 199
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atent No. 5658788
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Word CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Berg et al.
TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disc
NUMBER OF SEQUENCES: 28
:: |:|||||||:||: :: | :: ||:|||||:||: :: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
                                                                                                                  RPQKTASNCYITGWG--DT-GRAYSRTLQQAAIPLLPKRFC-EERYKGR-FTGRMLCAGN
                                                                                                                                                                                       LQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGD 288
                                                                                                                                                                                                                                                        TLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRE 703
                                                                                                                                                                                                                                                                                                                                                                                 GGWPWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHCFK-RYGNSTRSYAVRVG-DYH 643
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OPERATING SYSTEM: M
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355 AA; 39563 MW; 638774 CN;
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Db 348 WIR 350 ||: Qy 815 WIK 817

Search completed: Mon Mar 13 10:10:06 2000 Job time : 23 secs.

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ddT protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:08:48 2000; MasPar time 32.43 Seconds 600.342 Million cell updates/sec

Title:

Description:
Perfect Score:
Sequence:

>US-09-147-947-6
(1-822) from US09147947A.pep (1 of 2)
6328
1 PTTRPPPPPLPRFPRPPRALP......PGVYTKVSAFVPWIKSVTKL 822

Scoring table: PAM 150 Gap 11

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

188963 seqs, 23686106 residues

Database:

a-geneseq35 1:geneseqp

Statistics: Mean 37.360; Variance 145.793; 'scale 0.256

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	% Query Match	Length	DB	ĬD	Description	Pred. No.
μ.	ωı	? :	NI I	ᆸ	0 1	Human serine protease	0.00e+00
N	6328	100.0	875	\vdash	8336	neurotrypsin.	. 00
ω	\mathbf{L}		₩.	\vdash	336	Mouse neurotrypsin.	
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10	605	•	N)	_	392	a (466-470) tPA	.02e-4
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12	599		N)	ب	391	66-470) tPA	.72e-4
13	598	•	K)	ب	48	466-470) tPA	.19e-4
14	600	٠	(п	ب	26	29 cell 1	.35e
15	597	٠	ŧπ	۳	691	d sequence	.79e-4
16	597	•	N)	ب	391	66-4	.79e-4
17	590		in	ப	58	ied tissue plas	.52e-4
18	588		10	Ь	90	rokinase deriv	.46e-4
19	586		ш	ب	79	se mutant	.99e-
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t-PA variant H432A, R4	Novel tissue plasminog	t-PA deletion variant	t-PA deletion variant	Sequence of coding reg	Pro-urokinase mutant S		Pro-urokinase mutant S	PUK G16A G17A.	PUK S26T.	PUK P34A.	PUK.		PUK Y24A.		PUK C32P.	PUK N32P G38K.	Pro-urokinase mutant S	PUK G16A.	PUK G38A G39A.	PUK N32P G38K G39K.	Human native prourokin
1.05e-46	. 23	6.46e-47	. 05		4		.05e-4	8.23e-47		8.23e-47	8.23e-47	8.23e-47	8.23e-47	.23e	8.23e-47	8.23e-47	. 23e	8.23e-47	8.23e-47	8.23e-47	6.46e-47

ALIGNMENTS

Db	Oy Db	Qy Qy	Qy Db	Qy Qy	M B Q	RESULT ADDES DDC DDC DDC DDC DDC DDC DDC
241 ELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGSGPVMLDEVRCTGNE 300	181 WSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCSFSHGPTFPIIRLAGGSSVHEGRV 240 	121 GGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGGKGIAKQTPFSGLGLIPIY 180 	61 EVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVDWGYCDCRHGSVRLR 120 	1 PTTRPPPPLPREPRPPRALPAQREHALQAGHTPRPHPWGCPAGEPWVSVTDEGAPCLRWA 60 	Query Match 100.0%; Score 6328; DB 1; Length 822; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 822; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	W99087 standard; Protein; 822 AA. W99087; 13-MAY-1999 (first entry) Human serine protease BSSP-3; brain tissue. Serine protease; BSSP-3; brain tissue. Homo Sapiens. W09905290-A1. 04-FEB-1999; 24-JUL-1998; J03324, 24-JUL-1998; J03324, 24-JUL-1997; JP-213969. (SUNR) SUNTORY LITD. TSURUOKA N, Yamaguchi N, Yamashiro K; WPI; 99-142942/12. TSURUOKA N, Yamaguchi N, Yamashiro K; WPI; 99-142942/12. New Serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Claim 1; Page 61-65; 69pp; Japanese. The present sequence is a serine protease designated BSSP-3, which is isolated from human brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs. Sequence 822 AA;

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RESULT
ID W
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New human and murine neurotrypsin - used, e.g. for inhibiting by tumours, treatment of neurological or lung disease, including by gene therapy and in drug development as Claim 1; Page 20-24; Sopp; English.

The present sequence represents human neurotrypsin. Neurotrypsin proteins and polynucleotides can be used: (i) to inhibit tumours, including can polynucleotides can be used: (i) to inhibit tumours, including can polynucleotides can be used: (i) to inhibit tumours, including can polynucleotides can be used: (i) to inhibit tumours, including can polynucleotides can be used: (i) to inhibit tumours, including can polynucleotides can be used: (i) to inhibit tumours, including can polynucleotides can be used: (i) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the commons of (iii) to treat or prevent neurodegeneration, can cause of hypoxia, concrease survival of damaged neurons (e.g. in cases of hypoxia, or estination, nerve transection) and to stimulate regeneration and/or can causes of cell death) in the nervous system; (vii) to regenerate brain causes of cell death) in the nervous system; (vii) to regenerate brain
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09849322-A1.
5-NOV-1998; IB0625.
24-APR-1997; CH-000966.
26-APR-1997; CH-000966.
(SOND/) SONDEREGGER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; neurotrypsin; tumour inhibition; neurological disease; lung disease; gene therapy; drug development; stroke; brain injury; neurodegeneration; neuroinflammatory disease; multiple sclerosis; epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;
                                                                                                                                                                                                                                                                                                                                              WPI; 99-009438/01.
N-PSDB; V72589.
                                                                                                                                                                                                                                                                                                                                                                                     Sonderegger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human neurotrypsin.
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          PGESWVYYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKSVTKL
                                                               GRAYSRTLQQAAIPLLPKRFCEERYKGRFTGRMLCAGNLHEHKRVDSCQGDSGGPLMCER
                                                                                                                                                   PGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKSVTKL
                                                  GRAYSRTLQQAAIPLLPKRFCEERYKGRFTGRMLCAGNLHEHKRVDSCQGDSGGPLMCER
                                                                                                                 IHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQKTASNCYITGWGDT
                                                                                                                                                                                                         DAGVICDYFGKKASGNSNKESLSSVCGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSS
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                                                                                                   IHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQKTASNCYITGWGDT
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l Similarity 100.0%;
822; Conservative
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The present sequence represents mouse neurotrypsin. Neurotrypsin proteins and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or retina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration, neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to increase survival of damaged neurons (e.g. in cases of hypoxia, causes of synapses; (v) to treat or prevent retinal disorders (e.g. degeneration of synapses; (v) to treat or prevent appptosis (or other causes of cell death) in the nervous system; (vii) to regenerate brain causes of cell death) in the nervous system; (vii) to improve brain performance, including learning and memory; (x) to treat or prevent a poptosis (v) to treat or prevent approve brain confidence, including learning and memory; (x) to treat or prevent approve brain or lung injury associated with protease expression (specifically emphysema or honory; (x) to treat brain or lung injury associated with protease expression (specifically emphysema or
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N-PSDB; V72590.
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24-APR-1998; IB0625.
26-APR-1997; CH-000966.
(SOND/) SONDEREGGER P.
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ACLPLWRERPQKTASNCHITGWGDTGRAYSRTLQQAAVPLLPKRFCKERYKGLFTGRMLC
                                          AVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLP
                                                              AVRVGDYHTLVPEEFEQEIGVQQIVIHRNYRPDRSDYDIALVRLQGPGEQCARLSTHVLP
                                                                                                                               KRIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSY
                                                                                                                                                                                                                CTGNERSLADCIKQDIGRHNCRHSEDAGVICDYFGKKASGNSNKESLSSVCGLRLLHRRQ
                                                                                                                                                                                                                                                                                                       KEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGKGPIHVDNVK
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larity 87.0%;
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Pred. No. 0.00e+00;
51; Mismatches 28
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Example 1, Page 51-54; 69pp; Japanese.

The present sequence is a Serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuruoka N, Yamaguchi N, WPI; 99-142942/12. N-PSDB; X19027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-1999.
24-JUL-1998; J03324.
24-JUL-1997; JP-213969.
(SUNR) SUNTORY LTD.
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Mouse serine protease BSSP-3; bra.
Serine protease; BSSP-3; bra.
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                                                     CDCGQGPALPVIRLVGGNSGHEGRVELYHAGQWGTICDDQWDNADADVICRQLGLSGIAK
                                                                                                                       CTGNEKALADCVKQDIGRHNCRHSEDAGVICDYLEKKASSSGNKEMLSSGCGLRLLHRRQ
                                                                                                                                                                        KEGRVEVFVNGQWGTICDDGWTDKHAAVICRQLGYKGPARARTMAYFGEGKGPIHMDNVK
                                                                                                                                                                                                                            WLDDVSCSGKEVSFIQCSRRQWGRHDCSHREDVGLTCYPDSDGHRLSPGFPIRLVDGENK
                                                                                                                                                                                                                                                                             LAGGKSTHEGRLEVYYKGQWGTVCDDGWTEMNTYVACRLLGFKYGKQSSVNHFDGSNRPI
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                           AVRVGDYHTLVPEEFEQEIGVQQIVIHRNYRPDRSDYDIALVRLQGPGEQCARLSTHVLP
                                                                                                        CTGNERSLADCIKQDIGRHNCRHSEDAGVICDYFGKKASGNSNKESLSSVCGLRLLHRRQ
                                                                                                                                                           KEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGKGPIHVDNVK
                                                                                                                                                                                                             WLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENK
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        66.4%;
llarity 87.0%;
Conservative
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Pred. No. 0.00e+00;
51; Mismatches 28
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for diagnosis and treatment of tumours

Claim 2: Fig 2: 54pp: German.

This sequence represents a human protein which contains a SRCR (scavenger receptor, cysteine-rich) domain. The gene and encoded protein can be used to diagnose or treat tumours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist and to assess the significance of individual forms on cellular properties. The protein can be used to detect the presence of autoantibodies and antibodies which regulate its expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins containing scavenger receptor, cyste useful for diagnosis and treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mollenhauer J, Pou
WPI; 98-399136/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JAN-1998; D00096.
18-JUL-1997; DE-0030997.
09-JAN-1997; DE-000519.
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment; ervous system; medullo-blastoma; glioma; breast; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W64591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9830687-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human SRCR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W64591 standard; Protein; 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                utoantibody; ss.
 372
                                    919
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                                                                                                                                                                                                                                             741
                                                                                                                                                                                                                                                                                175
                                                                                                                                                                                                                                                                                                                                                   116
                                                                                                                                                                                                                                                                                                                                                                                 622 ALRLVNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWAMSAPGNARF-GQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
CRQLGFKYGKQASAN-HFEESTGPIWLDDVSCSGKETRFL-QCSRRQWGRHDCSHREDVS
                CRQLGCGWAMSAPGNAQFGQGSGPIVLDDVRCSGHES-YLMSCPHNGWLSHNCGHHEDAG
                                                                                                                                                                                                                             ASTAGSESSLALRLYNGGDRCQGRVEVLYR-GSWGTVCDDYWDINDANVVCRQLG-CGWA 798
                                                                                                                                                                                                                                                                                                              GSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQPTPSPDTWPTSH 740
                                                                                                                                      AKAWHQAYFGEGSGPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT----P
                                                                                                                                                                                                           L--AGG-SS----VH--E---GRVE-LYHAGQWGTVCDDQWDDADAEVICRQLGLSG-I
                                                                    L-T-DG--VIRL--AGG----
                                                                                                   TPSPDTWPTSRASTAGSESTLALRLVNGGDRCRGRVEVLYQGSWGTVCDDYWDTNDANVV
                                                                                                                                                                        TSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQP
                                                                                                                                                                                                                                                                              GLIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS-F-SH---GP-TFPIIR
                                                                                                                                                                                                                                                                                                                                                 SVRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLG-GKGIAKQTPFSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                        207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 781; DB 1;
Pred. No. 9.17e-68;
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                                                                 -GS-H-EGRLEVYYRGQWGTVCDDGWTELNTYVV
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1785;
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Matches

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Indels 24;

Gaps 83 283

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                                                                                                                                             cysteine-rich (SRCR) family. The sequence was deduced from an isolated CDNA clone (see V54605). Sp alpha transcripts are found in human bone marrow, spleen, lymph node, thymus and foetal liver but not in non-lymphoid tissues. Sp alpha has the same domain corganisation as the extracellular region of CD5 and CD6 and is composed of 3 SRCR domains. It is capable of binding to cells of the monocytic lineage, and appears to be involved in the regulation of monocyte activation, function and/or survival, and is therefore an important component in the immunoregulatory system. Methods of recombinantly producing Sp alpha are disclosed. In addition, antibodies reactive with Sp alpha are provided, as are methods of using antibodies that bind to Sp alpha for modulating the interaction between Spalpha and its receptor. Sp alpha can be used
                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                         which can be used to modulate the immune response claim 7; Fig 1A-B; 46pp; English.

This is the amino acid sequence of a novel protein (see W682) termed SP alpha, that is a member of the scavenger receptor cysteine-rich (SRCR) family. The sequence was deduced from isolated CDNA clone (see V54605). SP alpha transcripts are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W68200 standard; Protein; 347
W68200;
07-DEC-1998 (first entry)
                                                                                               in pharmaceutical compositions to regulate the immune response for example, autoimmune disease, viral infections, transplant rejection suppression, tumour cell proliferation suppression, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SP alpha; scavenger receptor; SRCR; immunomodulator; autoimmune disease;
                                                                      combined variable 
Sequence 347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAR-1997; US-039956
(BRIM ) BRISTOL-MYERS SQUIBB C
Aruffo AA, Gebe JA, Siadak AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1998;
06-MAR-1997;
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11.5%;
ilarity 40.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
ger receptor p
                                                                                                                                                                                                                                                                                                                                                                                                                               receptor cysteine-rich protein
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245. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=
                                                                      immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "cysteine-rich domain"
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64; M
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SRCR; human; antibody; immunoassay;
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   re 729; DB 1; Le
1. No. 3.12e-62;
Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transplant rejection; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain"
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RESULT RESULT AC Y.Y. 
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27 - OCT - 1997

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29 - OCT - 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-thrombotic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y13369 standard; Protein;
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24-OCT-1997;
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US-063704.
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US-063550.
US-063564.
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US-062814

US-062816

US-063045

US-063120

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US-065444
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with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzhelmer's disease, Als, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO530 can be used as an anti-thrombotic agent; PRO370 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood reseals, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-1997;
(GETH ) GENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH
Chen J, Goddard A,
WPI; 99-229533/19.
                                                                                                                                                                                                                                         associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated
                                                                                                                                                                                                                                                                                                                  Y13344-403 represent secreted and transmembrane human proteins. The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology known polypeptides, e.g. PRO211 and PRO217 can be used for disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; X52240.
New isolated human
 sequence
                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal ulceration
Claim 12; Fig 54; 320pp; En
Y13344-403 represent secret
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31-OCT-1997;
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347 AA;
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US-066770.
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US-066772.
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B Qy 밁 Q 밁 Q В Qy Вp δÃ В Matches Query Match 313 456 396 202 338 142 284 227 84 VRCSGEEQSLEQCOHRFWGFHDCTHQEDVAVIC KEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGY-KGPARA-RTMAYFGEGKGPIHVDN CSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWLDN GGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLG-FKYG-KQASANHFEESTGPI IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLG-LSGIAKAWHQAY--FG WLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENK WLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVEC----ED---P--FDLRLVGGDNL DGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVLTQKRCNKHAYGRKPI EGSGPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSC-TPLTD-G-V---IRLA EKEQKVLIQSVSCTGTEDTLAQCEQEE - - VYDCSHDEDAGASCENPESSFSPVPEGVRLA 141 11.5%; 11 Similarity 40.5%; 135; Conservat Score 729; DB 1; Le Pred. No. 3.12e-62; 64; Mismatches 110; 345 Length 347; Indels 24; Gaps 455 395 201 337 283 14;

VKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC

Search completed: Mon Mar 13 10:09:25 2000 Job time : 37 secs.

Post-processing:	Searched:	Scoring table:	Title: Description: Perfect Score: Sequence:	Tabular output not generated	Run on:	h_pp prot	Releas Copyri	**
Minimum Match 0% Listing first 45 summaries	142080 segs, 47172406 residues	РАМ 150 Gap 11	>US-09-147-947-6 (1-822) from US09147947A.pep (1 of 2) 6328 1 PTTRPPPPPLPRFPRPPRALPPGVYTKVSAFVPWIKSVTKL 822		Mon Mar 13 10:07:35 2000; MasPar time 51.90 Seconds	protein - protein database search, using Smith-Waterman algorithm	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 49.212; Variance 79.920; scale 0.616

Statistics:

Database:

pir62
1:pir1 2:pir2 3:pir3 4:pir4

RESULT ENTRY TITLE ORGANISM DATE

JC5759. #type complete
brain-specific serine proteinase (EC 3.4.21.-) - mouse
#formal_name Mus musculus #common_name house mouse
24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change
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t-plasminogen activat	acrosin (EC 3.4.21.10	low-density lipoprote	noge	.4.21.1	inogen act:	3.4.21	n (EC 3.4.2)	kallikrein	rein	en activa	1 (EC 3.4.21	ikrein (clone pGM7	פַ	_	antigen ((e	9	scavenger receptor cy	in-specif	Description		
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ALIGNMENTS

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AWHQAHFGEGSGPILLDEVRCTGNEMSIEQCPKSSWGEHNCGHKEDAGVSCVPLTDGVIR 274	CDCGQGPALPVIRLVGGNSGHEGRVELYHAGQWGTICDDQWDNADADVICRQLGLSGIAK 214 :: :: : : :	h 66.3%; Score 4195; DB 2; Length 761; .Similarity 86.8%; Pred. No. 0.00e+00; 527; Conservative 52; Mismatches 28; Indels 0; Gaps 0;	predicted\ #active_site His, Asp, Ser #status predicted #length 761 ##olecular-weight 84136 #checksum 5449	predicted #label SKC\ #domain furin binding #status predicted #label FRB\ #domain trypsin homology #label TRY\ #binding_site carbohydrate (Asn) (covalent) #status	# C.	•	#domain kringle-like #status predicted #label KRI\	<pre>cysteine-rich domain homology qlycoprotein; hydrolase; serine proteinase</pre>	##experimental_source brain FICATION	##cross-references DDBJ:D89871	ype mRNA 1~761 ##label YAM	JC5759	cysteine-rich motifs.	ם ב	"Sujimura, A.; Yamaguchi, N. Biochem. Biophys. Res. Commun. (1997) 239:386-392	Yamamura, Y.; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.;	JC5759 . JC5759 .

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#length
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Immunogenetics (1999) 49:773-786
Origins of immunity: transcription factors and homologs
effector genes of the vertebrate immune system express
                                                                                                                                                                                                                                                                                                                                                                    scavenger receptor cysteine-rich protein precursor - see urchin (Strongylocentrotus purpuratus)
#formal_name Strongylocentrotus purpuratus #common_name purple urchin
20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
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Eur. J. Immunol. (1993) 23:2320-2325
A new macrophage differentiation antigen the scavenger receptor superfamily.

nees MUID:93380506
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M130 antigen - human
#formal_name Homo sapiens #common_name man
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journal Eur. J. Immunol. (1993) 23:2320-2325
title A new macrophage differentiation antigen which the scavenger receptor superfamily.
ross-references MUID:93380506
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Similarity 39.2%;
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A new macrophage differentiation antigen which
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M130 antigen (cytosolic variant 1) - human
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                                                        #domain scavenger
#label SRC5\
                                                                                                                                                                                                                                                                                                                                                 preliminary; translated from GB/EMBL/DDBJ
                                     #domain scavenger receptor
                                                                                                           #domain scavenger
                                                                                                                                                                                 #domain scavenger receptor
                                                                                                                                               #domain scavenger
                                                                                                                                                                                                     #domain scavenger receptor cysteine-rich
#label SRC1\
                                                                                            #label SRC4\
                                                                                                                                #label SRC3\
                    #label SRC6\
                                                                                                                                                                   #label SRC2\
   scavenger
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Pred. No. 6.78e-199;
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                                                                         receptor
 cysteine-rich
                                     cysteine-rich domain
                                                                         cysteine-rich
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Matches 171; Conservation
                                                                                                                                                                                                                                                                                       #title the scavenger receptor superfamily. #cross-references MUID:93380506
                             365-468
                                                                258-361
                                                                                                    151-254
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                                                                                                                                                                                                                                                                                                                                                                                                             INCE
INCE
                                                                                                                                                                                             ##residues 1-1156 ##label RES
##cross-references EMBL:Z22970; NID:g312145; PID:g312146
#FICATION #superfamily scavenger receptor cysteine-rich domain homology
                                                                                                                                                                                                                                              ""status preliminary; translated from GB/EMBL/DDBJ##molecule_type mRNA##rasidno-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 SGRI-WMDHVSCRGNESALWDCKHDGWGKHSNCTHQQDAGVTCS--DGSNLEM-RLTRGG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 LRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAVSVICNQLG-CPTAIKAPGWANSSAG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WGGLTCDHYEEAKITC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENKKEGRVEVFINGQWGT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCTPLTDGVIRLAGGKGSHEGRLEVYY 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCKHHEWGKHYCNHNEDAGVTC-SDG-SD-LEL----RLRGGGSRCAGTVEVEIQRLLGK 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGOWGTVCDDGWTELNTYVVCRQLGFKYGKQASAN-HFEESTGPIWLDDVSCSGKETRFL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGEWGTICDDGWDSYDAAVACKQLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVW 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NMCSGRIEIKFQ-GRWGTVCDDNFNIDHASVICRQLE-CGSAVSFSGSSNFGEGSGPIWF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQT-PFSGLG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGKGPIHVDNVKCTGNERSLADCIKQD 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I38005 #type complete
M130 antigen (cytosolic variant 2) - human
#formal_name Homo sapiens #common_name man
17-May-1996 #sequence_revision 17-May-1996 #text_change
07-Feb-1997
                                                                                                                                                                             cytosol
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#domain scavenger receptor cysteine-rich domain homology
#label SRC8\
#domain scavenger receptor cysteine-rich domain homology
                                         #domain scavenger receptor cysteine-rich domain homology #label SRC3\
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                         scavenger receptor cysteine-rich domain homology
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Pred. No. 6.78e-199;
73; Mismatches 172; Indels 20; Gaps 16;
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* * * * *	acce ##	ACCESSIONS REFERENCE #authors #journal #title		ORGANISM	RESULT ENTRY TITLE	Qy 53	Db 45	Qy 47	Db 39	Qy 41	Db 33	Qу 35	Db 27	Db 21 Qy 29	Оу 23	Db 16	Qy 17	Db 10	Db 4 Qy 11	Query Best L Matche	SUMMARY	921-1	816-9	711-8	575-67	470-5
residues cross-refe note note	eferer on ecule			_	7	1 IGRHNCRI	2 WGGLTCDI	1 ICDDGWTI	2 VCDRGWGI	1 QCSRRQWGR	9 ОСКННЕМ	2 RGQWGTV		2 9	4 SVHEGRVI	1 NMCSGRIE	6 LIPIYW-	5 SGRI-WM	6 LRLVDGENKC : 7 VRLRGGKNEF	Match ocal Simi s 171;	_	024	20	814	78	73
: 1-352,'G',354-532 ##label DA2 :ferences GB:J04518 the authors translated the codon CAC for residue 353 as Gly part of this sequence was confirmed by protein sequencing	egg peptide speract. ces MUID:89184581 A32751 type mRNA	A32/51; A3120/ A32/51 A32/51 Dangott, L.J.; Jordan, J.E.; Bellet, R.A.; Garbers, D.L. Proc. Natl. Acad. Sci. U.S.A. (1989) 86:2128-2132 Cloning of the mRNA for the protein that crosslinks to the	03-Aug-1922 #sequence_revision 03-Aug-1992 #text_change 02-Aug-1996	<pre>purpuratus) #formal_name Strongylocentrotus purpuratus #common_name nurple urchin</pre>	A32751 #type complete speract receptor precursor - sea urchin (Strongylocentrotus	RHNCRHSEDAGVIC 546	WGGLTCDHYEEAKITC 467	DDGWTDKDAAVICRQLGYKGPARARTMAYFGEGKGPIHVDNVKCTGNERSLADCIKQD 530	CRQ	HDCSHREDVSIACY	KHHEWGKHYCNHNEDAGVTC-SDG-SD-LELRLRGGGSRCAGTVEVEIQRLLGK 391	RGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASAN-HFEESTGPIWLDDVSCSGKETRFL 410	CDDGWDSYDAAVAC	DDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRF 278	EL-YHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWH-QAYFGEGSGPVM	<pre>IKFQ-GRWGTVCDDNFNIDHASVICRQLE-CGSAVSFSG : :: : : :</pre>	SNVRCRGDEENILLCEKDIW-QGGVCPQKMAAAVTCSFSHGPTFPIIRLAGGS 233	WMDHVSCRGNESALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEM-RLTRGG 160	VDGENKCSGRVEVKVQEEWGTVCNNGWSMEAVSVICNQLG-CPTAIKAPGWANSSAG 104 	14.9%; Score 946; DB 2; Length 1156; ilarity 39.2%; Pred. No. 6.78e-199; Conservative 73; Mismatches 172; Indels 20; Gaps 16;	#length 1156 #molecular-weight 125352 #checksum 9043	ro.	#Label SMC/\ #domain scavenger receptor cysteine-rich domain homology #label CBCON	#Label SRCb\ #domain scavenger receptor cysteine-rich domain homology		

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CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t Local Similarity 33.5%;
thes 151; Conservative
                                                                                                                                                                                                                                         278 EIWHDDAWGTICDDGWDWADANVVCRQAGYRGAVKASGFKGEDFGFTWAPIHTSFVMCTG 337
|: |||:|||| :: ||||| |:: ||: ||: || ||:|
348 EVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEE-S-T-GPIWLDDVSCSG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 GNER-SLADCIKODIGRHNCRHSEDAGVICD 547
                                                                             396 VSLGNGWGRVCDPDWSDHEAKTVCYHAGYKWGASRAAGSAEVSAPFDLEAPFIIDGITCS 455
                                                                                                                                                           405 KETRFLQCSRRQ-WGRHDCSHREDVSIACYPGGEGHRLSLGF-PVRL-MDGENKKEGRVE 461
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                                                                                                                                                                                                                                                                                                                                                                                                      100 -AHVITEWYKMNCIGNETRLEDCYHRPYGRPWLCNAQWAAGVECLPKDEPQGSL;RMIL 157
                                     456 GVENETLSQCQMKVSADMTCA-TGDVGVVCE 485
                                                                                                                                                                                                                                                                                                                                                            218 LDAVDCEGTEAHITECNMPVTPYQHACPYTHNWDVGVVCKPNVEGDIRLMDGSGPHEGRV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 LGLIPIYWS-NVRCRGDEENILLC-EKDIWQGGVCPQKMAAAVTCSFSHGPTFPIIRLAG 231
                                                                                                                                                                                  VEDRLIDCILRDGWT-HSCYHVEDASVVC-ATDDDDTIEIEPKHTRVRIVGMGQGGRVE 395
                                                                                                                                                                                                                                                                                                                        *superfamily scavenger receptor cysteine-rich domain homology membrane protein
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#product speract receptor #status predicted #label MAT\
#domain scavenger receptor cysteine-rich domain homology
#label SRC1\
#domain scavenger receptor cysteine-rich domain homology
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#label SRC4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 852; DB 2; Length 532;
Pred. No. 4.36e-175;
99; Mismatches 177; Indels 24; Gaps
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Search completed: Mon Mar 13 10:08:30 2000 Job time: 55 secs.

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dd_h protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:04:57 2000; MasPar time 33.12 Seconds $741.229 \ \mathrm{Million}$ cell updates/sec

Description: Perfect Score: Title:

Sequence: >US-09-147-947-6
(1-822) from US09147947A.pep (1 of 2)
6328
1 PTTRPPPPLPRFPRPPRALP......PGVYTKVSAFVPWIKSVTKL 822

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 50.140; Variance 71.058; scale 0.706

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8.68e-109	2.70e-111	.72e-	2.07e-112	1.21e-114	8.37e-121	1.21e-121	3.58e-124	1.31e-123	9.09e-123	9.09e-123	3.09e-129	3.09e-129	2.16e-128	1.13e-128	6.28e-131	2.30e-130		2.38e-196	2.16e-200	0.00e+00	0.00e+00	Pred. No.

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44 45	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
483	485	488	488	487	493	496	493	499	504	512	512	514	512	513	516	519	520	518	519	526
7.6	7.7	7.7	7.7	7.7	7.8	7.8	7.8	7.9	8.0	8.1	8.1	8.1	8.1	8.1	8.2	8.2	8.2	8.2	8.2	8.3
492	810	786	583	434	812	810	432	593	433	1019	812	655	468	343	477	477	433	431	338	1069
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TMS2_HUMAN	PLMN_MACMU	STUB_DROME	CFAI_HUMAN	UROK_CHICK	PLMN_MOUSE	PLMN_HUMAN	UROK_RAT	FA12_BOVIN	UROK_MOUSE	ENTK_HUMAN	PLMN_BOVIN	HGFA_HUMAN	CD6_HUMAN	PLMN_SHEEP	URT2_DESRO	URT1_DESRO	UROK_BOVIN	URTB_DESRO	PLMN_HORSE	ENTK_MOUSE
CHYMOTRYPSIN-LIKE PROT TRANSMEMBRANE PROTEASE	PLASMINOGEN PRECURSOR	SERINE PROTEINASE STUB	COMPLEMENT FACTOR I PR	UROKINASE-TYPE PLASMIN	PLASMINOGEN PRECURSOR	PLASMINOGEN PRECURSOR	UROKINASE-TYPE PLASMIN	COAGULATION FACTOR XII	UROKINASE-TYPE PLASMIN	ENTEROPEPTIDASE PRECUR	PLASMINOGEN PRECURSOR	HEPATOCYTE GROWTH FACT	T-CELL DIFFERENTIATION	PLASMINOGEN (EC 3.4.21	SALIVARY PLASMINOGEN A	SALIVARY PLASMINOGEN A	UROKINASE-TYPE PLASMIN	SALIVARY PLASMINOGEN A	PLASMINOGEN (EC 3.4.21	ENTEROPEPTIDASE (EC 3.
9.11e-96 9.11e-96			3.81e-97	7.18e-97	1.58e-98	2.35e-99	1.58e-98	3.48e-100	1.44e-101	8.71e-104	8.71e-104	2.43e-104	8.71e-104	4.60e-104	6.76e-105	9.94e-106	5.24e-106	1.88e-105	9.94e-106	1.13e-107

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AJ001531; CAA04816.1; - E; PS00134; TRYPSIN_HIS E; PS00135; TRYPSIN_SER E; PS00420; SPERACT_REC ase; Serine protease; G 1 20 170 271 280 381 387 487	This SWISS-PROT entry is copyri- between the Swiss Institute of the European Bioinformatics Ins- use by non-profit institution modified and this statement is a entities requires a license agr- or send an email to license	UENCE FROM N.A. UES-BRAIN; LINE; 98201705. AK., GSCHWEND T.P., SONDEREGG ning and sequencing of the cDN him. Biophys. Acta 1396:143-14 FUNCTION MAY SUBSERVE STRUCTURAL LEARNING AND MEMORY OPERATIONS SUBCELLULAR LOCATION: SECRETED SIMILARITY: BELONGS TO PEPTIDA TRYPSIN FAMILY.	STAND (Rel. 39 (Rel. 39 (Rel. 39 PRECURS PRECURS (Human) etazoa; imates;
A04816.1; TRYPSIN_HIS; 1. TRYPSIN_SCR; 1. SPERACT_ENCEPTOR; 3. PIOTEASE; Glycoprotein; Kringle; Repeat; Signal. 20 POTENTIAL. 875 NEUROTRYPSIN. 92 PROLINE-RICH. 165 KRINGLE. 271 SRCR 1. 381 SRCR 2. 487 SRCR 3.	copyright. It is producte of Bioinformatics Institute. There its Institute. There its Institute as long as ant is not removed. Unse agreement (See htt see@isb-sib.ch).	UENCE FROM N.A. (UE-BRAIN; (UE-BRAIN; (UE-BRAIN; (UE-BRAIN; AK., GSCHWEND T.P., SONDEREGGER P.; ning and sequencing of the cDNA encoding human neurotrypsin."; him. Biophys. Acta 1396:143-147(1998). FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC FUNCTION MAY SUBSERVE STRUCTURAL REDREAMIZATIONS ASSOCIATED WITH LEARNING AND MEMORY OPERATIONS (BY SIMILARITY). SUBCELULLAR LOCATION: SECRETED. SUBCILULAR LOCATION: SECRETED. SUBCILULAR LOCATION: SECRETED. SUBCILULAR LOCATION: SECRETED. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYBEIN FAMILY. SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.	ARD; PRT; 875 AA. Created) Last sequence update) Last annotation update) CR (EC 3.4.21) (MOTOPSIN). Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.

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PGESWYVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKSVTKL
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EMBL; D89871; BAA23986.1;

MGD; MG1:1100881; PRSS12;

PFAM; PF00530; SRCR; 3.

PFAM; PF00089; trypsin; 1.
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GSCHWEND T.P., KRUEGER &

"Neurotrypsin, a novel m

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MOL. Cell. Neurosci. 9:2
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NEUROTRYPSIN PRECURSOR (EC 3.4.21.-)
PROTEASE 3) (BSSP-3).
PRSC17
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SIGNAL
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SUBCELLULAR LOCATION: SE
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FUNCTION: PLAYS A ROLE REURONAL PLASTICITY A ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS LEARNING AND MEMORY OPERATIONS.
TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL C
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TRYPSIN_SER; 1.
SPERACT_RECEPTOR;
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          of a novel brain-specific serine ture and three scavenger receptor
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3.4.21.-) (MOTOPSIN)
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SERINE PROTEASE.

ZYMOGEN ACTIVATION REGION.

REACTIVE BOND (POTENTIAL).

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

POTENTIAL.

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Best Local
                                       SEQUENCE FROM N.A., AND SEQUENCE OF 477-489.
MEDLINE; 89184.581.

DANGOTT L.J., JORDAN J.E., BELLET R.A., GARBERS D.
"Cloning of the mRNA for the protein that crosslin
peptide speract.";
Proc. Natl. Acad. Sci. U.S.A. 86:2128-2132(1989).
-: FUNCTION: RECEPTOR FOR THE EGG EDETIDE SPERACT
-: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                               SPER_STRPU STANDARD; PRT; 53
P16264;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence upd
15-JUL-1999 (Rel. 38, Last annotation u
EGG PEPTIDE SPERACT RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
      This SWISS-PROT
                                                                                                                                                                                                                                              Strongylocentrotus.
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51; Mismatches 28
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PFAM; PF00530; SRCR;
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Pred. No. 2.16e-200;
99; Mismatches 177;
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Bos taurus Eukaryota;

(Bovine). Metazoa;

Chordata;

Craniata;

Vertebrata;

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Query Match
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PIR; S19913; S19913.
PIR; A46496, A46496.
PROSITE; PS00420; SPERACT_RECEPTOR;
PFAM; PF00530; SRCR; 11.
 SEQUENCE FROM N.A MEDLINE; 86243360 FUJIKAWA K., CHUNG
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Eukaryota; Metazoa; (
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133; Conser
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(Rel. 02, Last sequence update)
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FACTOR XI PRECURSOR (EC 3.4.21.27)
(PTA).
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     CHUNG
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   D.W.,
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     HENDRICKSON
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Pred. No. 2.38e-196;
64; Mismatches 120;
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     DAVIE
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Blood 79:1435-1440(1992).
-!- FUNCTION: FACTOR XI TRIGGERS THE MIDDLE PHASE OF
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MCMULLEN B.A., FUJIKAWA K., DAVIE E. "Location of the disulfide abonds in presence of tandem apple domains."; Biochemistry 30:2056-2060(1991).
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MEIJERS J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 88107663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prekallikrein
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Jews is a bleeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Amino acid sequence of human factor XI, with four tandem repeats that are highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASAKAI R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ARIANT LEU-301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Organization
                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBI European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and fine the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY OF BLOOD COAGULATION BY ACTIVATING FACTOR IX.

CATALYIC ACTIVITY: SELECTIVE CLEAVAGE OF ARG-1-ALA AND ARG-1-VAI
BONDS IN FACTOR IX TO FORM FACTOR IXA.

SUBUNIT: HOMODIMER: LINKED BY A DISULFIDE BOND. AFTER ACTIVATION
THE HEAVY AND LICHT CHAINS ARE ALSO LINKED BY A DISULFIDE BOND.
THE HEAVY AND LICHT CHAINS ARE ALSO LINKED BY A DISULFIDE BOND.

PTM: ACTIVATED BY FACTOR XIIA (OR XII), WHICH CLEAVES EACH
POLYPEPILDE AFTER ARG-387 INTO THE LIGHT CHAIN, WHICH CONTAINS THE
ACTIVE SITE, AND THE HEAVY CHAIN, WHICH ASSOCIATES WITH HIGH
                   ; A27431; K
P; P00763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASHKENAZI JEWS.
SIMILARITY: CONTAINS 4 APPLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVE SITE, AND AND MOLECULAR WEIGHT (HMW) KININOGEN.
DISEASE: DEFECTS IN FII ARE A CAUSE OF A BLOOD
DISEASE: DOFENTHAL SYNDROME) OCCURRING IN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYPSIN FAMILY. BELONGS TO THE PLASMA KALLIKREIN SUBFAMILY.
                                                      M18301;
M18302;
M18303;
M18304;
M19417;
M20217;
                                                                                                                                                                                                         M18298;
                                                                                                                                                                                                                                                M18296;
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                                                                                                                                                                                                                                                                                                                                             requires a license agreement
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                                                                                                                                                                                                                                                                                                                          email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAVIE E.W.,
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                                     KFHU1
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                     1DPO
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AAA51985.1;
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                                                                                                                                                                                                                                                                                                                            to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND DISULFIDE BONDS
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                                                                        JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a blood coagulation factor homologous with plasma
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CARBOHYD
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PROSITE;
PROSITE;
PROSITE;
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Duplication; Signa
SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00024; apple; 4. PFAM; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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               614 YVDWI
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ITE; PS00134; TRYPSIN_HIS;
ITE; PS00135; TRYPSIN_SER;
ITE; PS00495; APPLE; 4.
                                                                                            RVYSGILNQSEIKED-TSFFGVQEIIIHDQYKMAESGYDIALLKLETTVN-YT--DSQR- 497
                                                                                                               RIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYG-NSTRSY 635
                                                                                                                        RIVGGTASVRGEWPWQVTLH-TTSPTQ-RHLCGGSIIGNQWILTAAHCF--YGVESPKIL 442
  FVPWI
                                         KMICAGY-REGGK-DACKGDSGGPLSC-KHNEVWHLVGITSWGEGCAQRERPGVYTNVVE
                                                                     PICLPSKGDR-NVIYTDCWVTGWGYRKLRDKIQNTLQKAKIPLVTNEECQKRYRGHKITH 556
                                                                                   AVRVGD-YHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVL 694
                            RMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSA 811
                                                       PACLPLWRERPQKTASNCYITGWG-DTGRA-YSRTLQQAAIPLLPKRFCEERYKG-RFTG
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               618
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625
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514
545
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301
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larity 42.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal;
                                                                                                                                                                        AA;
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al; Disease mutation.
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70109
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581
560
599
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Pred.
53; M
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/FTId=VAR_006622.
C -> S (IN REF. 2).
; C46A5F74 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                       APPLE 1.
APPLE 2.
APPLE 3.
APPLE 4.
CATALYTIC.
                                                                                                                                                                                                                                     INTERCHAIN.
                                                                                                                                                                                                                                                                                                                                  WITH A CYS RESIDUE
                                                                                                                                                                                                                                                                                                                                                                                                                                           COAGULATION COAGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                               634; DB 1; I
NO. 5.45e-138;
Wismatches 71:
                                                                                                                                                                                                                                       (BETWEEN HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                           FACTOR
                                                                                                                                                        Length 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                         XIA HEAVY CHAIN.
XIA LIGHT CHAIN.
                                                                                                                                           Indels
                                                                                                                                                                                                                                      AND LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coagulation;
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                                                                                                                                           Gaps
                                         613
                                                       751
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HSSP; P00750; 1RTF.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00125; EGF_1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS0123; FIBRONECTIN_1; 1.

PROSITE; PS0123; FIBRONECTIN_1; 1.

PROSITE; PS00071; KRINGLE_1; 1.

PROSITE; PS00070; KRINGLE_2; 2.

PFAM; PF00008; EGF; 1.

PFAM; PF00008; Kringle; 2.

PFAM; PF00089; trypsin; 1.

PFAM; PF00089; trypsin; 1.

PFAM; PF00089; trypsin; 1.

PFAM; PF00089; trypsin; 1.
  DOMAIN
DOMAIN
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ACT_SITE
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DISULFID
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                                                                                                                                                                                                                                                                                                                             SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence upd
01-NOV-1997 (Rel. 35, Last annotation u
TISSUE PLASMINOGEN ACTIVATOR PRECURSOR
(T-PLASMINOGEN ACTIVATOR).
                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UROT_BOVIN STA
Q28198;
01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                          Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and tPA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAILY J. 5:605-617(1995).

FUNCTION: TPA CONVERTS PLASMINOGEN TO PLASMIN BY HYDROLYZING A SINGLE R-V BOND IN PLASMINOGEN. ACTIVE IN TISSUE REMODELING AND SINGLE R-V BOND IN PLASMINOGEN. ACTIVE IN EIBRINOLYSIS, AND IN CELL MIGRATION. PARTICULARLY IN FIBRINOLYSIS, AND IN CELL MIGRATION. CAPALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN PLASMINOGEN TO FORM PLASMIN.

MISCELLANEOUS: TPA ATTACHES TO THE KRINGLE STRUCTURE OF THE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-I DOMAIN.
SIMILARITY: CONTAINS 2 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY $1; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN OF FIBRIN.
                                                                                                                                                                                                                                                                                                                                                     Kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BERGLUND L., PETERSEN T and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cetartiodactyla; Ruminantia;
  40
83
128
219
361
410
517
517
70
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                                                                                                                                                                                                                                                                                                                                                                          EGF-like
    82
121
209
300
361
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517
72
79
                                                                                                                                                                                                                                                        566
                                                                                                                                                                                                                                                                                                     314
                                                                                                                                                                                                                                                                                                                             21
33
                                                                                                                                                                                                                                                                                                                        domain; Signal.
BY SIMILARITY.
BY SIMILARITY.
EGF-LIKE.

KRINGLE 1.

KRINGLE 2.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                          TISSUE PLASMINOGEN ACTIVATOR (LIGHT, SERINE PROTEASE). FIBRONECTIN TYPE-I.
                                                                                                                                                                                                                                                                                                   TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                             (HEAVY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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tion update)
Theore (EC 3.4.21.68) (TPA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA.
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                                                                                                                                                                                                                                                                                                   ACTIVATOR A CHAIN
                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
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RESULT
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)1-MAY-1992 (Rel. 2
)1-NOV-1997 (Rel. 3
PLASMA KALLIKREIN F
(KININGGENIN) (FLET
MEDLINE: 91090844.

SELDAH N.G., SAWYER N., HAMELIN J., MION P., BEAUBIEN G.,

BRACHPAPA L., ROCHEMONT J., MBIKAY M., CHRETIEN M.;

BRACHPAPA L., ROCHEMONT J., MBIKAY M., CHRETIEN M.;

"Mouse plasma kallikrein: cDNA structure, enzyme characterization
and comparison of protein and mRNA levels among species.";

and comparison of protein and mRNA levels among species.";

DNA Cell Biol. 9:737-748(1990)

-i- FUNCTION: THE ENZYME CLEAVES LYS-ARG AND ARG-SER BONDS. IT
ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BIN
TO A NEGATIVELY CHARGED SURFACE. IT ALSO RELEASES BRADYKININ
HMW KININGEN AND MAY ALSO PLAY A ROLE IN THE RENIN-ANGIOTENS
SYSTEM BY CONVERTING PRORENIN INTO RENIN.
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aryota; Metazoa; Chordata; Craniata; Vej
aryota; Rodentia; Sciurognathi; Muridae;
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63701
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22, Last sequence update)
35, Last annotation update)
PRECURSOR (EC 3.4.21.34) (PLASMA
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2.30e-130;
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ae; Murinae;
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Mus.
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RIVGGTNASLGEWPWQVSLQVKLV-SQTHL-CGGSIIGRQWVLTAAHCFDGIPYPDVWRI

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YGGILS-L-SEITKETPSSR-IKELIIHQEYKVSEGNYDIALIKLQTPLN-YTEF--QK-RIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFK--RYGNSTRS

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Query Match
Best Local s
Matches 10
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PROSITE; PS00134; TRYPSIN_HIS;

PROSITE; PS00135; TRYPSIN_SER;

PROSITE; PS00495; APPLE; 4.

PFAM; PF00024; apple; 4.
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                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibrinolysis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: THE ZYMOGEN IS ACTIVATED BY FACTOR XIIA, WHICH CLEAVES THE MOLECULE INTO A LIGHT CHAIN, WHICH CONTAINS THE ACTIVE SITE, AND A HEAVY CHAIN, WHICH ASSOCIATES WITH HAW KININGGEN. THESE CHAINS ARE LINKED BY ONE OR MORE DISULFIDE BONDS.

SIMILARITY: CONTAINS 4 APPLE DOWAINS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. BELONGS TO THE PLASMA KALLIKREIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A36557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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 l Similarity
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                                                                      Bradykinin.
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813	61:	75:	560	69	50:	63.
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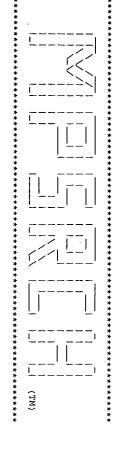
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Run on: protein - protein database search, using Smith-Waterman algorithm Mon Mar 13 10:05:52 2000; MasPar time 80.04 Seconds 712.069 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-09-147-947-6 (1-822) from US09147947A.pep (1 of 2) 6328

Sequence: 1 PTTRPPPPLPRFPRPPRALP......PGVYTKVSAFVPWIKSVTKL 822

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Pest-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl12
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 49.210; Variance 76.258; scale 0.645

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PLATELET FACTOR XI.	SCAVENGER-RECEPTOR PRO	SP-ALPHA.	SP-ALPHA.	TUNICATE RETINOIC ACID	SP ALPHA.	DMBT1/6KB.1 PROTEIN PR	DMBT1 PROTEIN.	SCAVENGER-RECEPTOR PRO	MUCIN (FRAGMENT).	HENSIN.	A SPERM-ACTIVATING PEP	SP85.	M130 ANTIGEN, CYTOPLAS	M130 ANTIGEN, CYTOPLAS	M130 ANTIGEN, EXTRACEL	M130 ANTIGEN PRECURSOR	SCAVENGER RECEPTOR CYS	SRCR DOMAIN, MEMBRANE	SCAVENGER RECEPTOR CYS	Description	
3.06e-126	6.76e-137	4.55e-141	4.95e-146	1.49e-146	5.27e-151	1.17e-164	4.98e-167	5.55e-171	6.67e-179	1.52e-181	1.99e-188	2.77e-190	2.40e-208	2.40e-208	2.40e-208	2.40e-208	1.15e-280	2.87e-299	0.00e+00	Pred. No.	

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6.77e-95	.77e-9	6.77e-95	.17e-	1.17e-95		.85e-9	5.71e-99	.17e-	.17e-	4.93e-102	.67e-	2.59e-103	.55e-	3.73e-107	.14e-	.94e-	.83e-	3.30e-109	.88e-	.72e-		1.13e-116	5e-	2.35e-122

ALIGNMENTS

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Query Match
Best Local S
Matches 19
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BLUMBACH B., PANCER Z., DIEHL-SEIFERT B., STE MUELLER I., MUELLER W.E.G.;

"The putative sponge aggregation receptor. Is characterization of a molecule composed of sc cysteine-rich domains and short consensus rep J. Cell Sci. 111:2635-2644(1998).

EMBL: Y14953; CAA75175.1; -.

PROSITE: PS00420; SPERACT_RECEPTOR; 8.
SEQUENCE 2043 AA; 220896 MW; 4CE19401 CRC
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096943;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-NOV-1999 (TrEMBLrel. 12, Last annotation
SECCE DOMAIN, MEMBRANE FORM 2.
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QCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENKKEGRVEVFINGQWGT
                                                                                                                                            ECSSSGLGQHNCQHFEDAGVECN-DHITPS-PVT-DLRLAGGTNATEGRVEIFFNNTWGT
                                                                        GQWGTVCDDGWTEL-NTYVVCRQLGFKYGKQASA-NHFEESTGPIWLDDVSCSGKETRFL
                                                                                                          KTWGTVCDDFW-DLGDATVVCRQLGYPEAVRAEPFARFGSGEGPIWLDDVACVGTETSLF
                                                                                                                                                                                   NVACTGFENSLDECRSNGWGDHNCGHREDAGAVCQGELLP-IRLRDGGSNLEGRVEVYFN
                                                                                                                                                                                                                     SSVHEGRVELYHAGOWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGSGPVMLD
                                                                                                                                                                                                                                          SGPHEGRVEIYYQGVWGTVCDDSWGQPDADVVCRQLGYANASRATVRAEFGRGTGEIWLD
                                                                                                                                                                                                                                                                                             GLGLIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCSFSHGPTFPIIRLAGG
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Pred. No. 2.87e-299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 150;
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repeats.";
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Best Local Similarity
Matches 199; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

PANCER Z., RAST J.P., DAVIDSON E.H.;

"Origins of Immunity: Transcription Fa

Vertebrate Immune System Expressed in

Immunogenetics 0.0-0(1999).

EMBL: AF076513: A0-00493.1;

HSSP; P56682; 1CCV.
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097378;
01-MAY-1999 (TIEMBLIE1. 10, Created)
01-MAY-1999 (TIEMBLIE1. 10, Last sequence update)
01-MOV-1999 (TIEMBLIE1. 12, Last annotation update)
SCAVENGER RECEPTOR CYSTEINE-RICH PROTEIN PRECURSOR.
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                   1016
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                                                                                                                                                                                                                                                      TIFDCAHPPFGVHNCAHYEDAGVVCIVS---Q----D--VRLVDGSNAAEGRVEIQYNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVGGSNEAEGRVEIQYNGVWGTICDDSWDITDASVVCRMLGFQGASGAPGSAQFGQGTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQDIGRHNCRHSEDAGVIC
                                                   HPPFGVHNCFHSEDAGVVC
                                                                                                                                                             WGTICDDFWDITDANVVCRMLGFQGASGAPGSAQFGQGTGPIQLDDVGCTGAEQTIFDCA
                                                                                                                                                                                                                      RFLQCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENKKEGRVEVFINGQ
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                                                                                                                                                                                                                                                                                                                                                                VMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCTPLTDGVIRLAGGKGSHEGRLE
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                                                                                                            WGT ICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGKGPIHVDNVKCTGNERSLADCI
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1036
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llarity 45.3%;
Conservative
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Pred. No. 1.15e-
84; Mismatches
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SCAVENGER RECEPTOR CYSTEINE-RICH MW; CBE8C531 CRC32;
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1.15e-280;
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01-NOV-1996
01-NOV-1999
M130 ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A new macrophage differentiation antigen scavenger receptor superfamily."; cur. J. Immunol. 23:2320-2325(1993). 2] BEQUENCE FROM N.A. BUBCHLER C., LANGMANN T., SCHMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic organization of the human CD163 gene."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases EMBL; Z22988; CAA80541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen;
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MASON D.Y.;
    411
                                                 339
                                                                                           352
                                                                                                                                                                                      292
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                                                                                    NMCSGRIEIKFQ-GRWGTVCDDNFNIDHASVICRQLE-CGSAVSFSGSSNFGEGSGPIWF 218
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                                                                                                                                                                                                      DDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRF 278
                                                                                                                                                                                                                                                                      SVHEGRVEL-YHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWH-QAYFGEGSGPVML 291
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    QCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENKKEGRVEVFINGQWGT
                                            QCKHHEWGKHYCNHNEDAGVTC-SDG-SD-LEL----RLRGGGSRCAGTVEVEIQRLLGK 391
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41 1116 M130 ANTIG
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Pred. No. 2.40e-208;
73; Mismatches 172.
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Eur. J. Immunol. 23:2320-2325(1993).
EMBL; Z22971; CAA80544.1; -.
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PRINTS; PR00258; SPERACTRCPTR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRF
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                                                                                                                                                                                                                                            QCKHHEWGKHYCNHNEDAGVTC-SDG-SD-LEL----RLRGGGSRCAGTVEVEIQRLLGK 391
                                                                                                                                                                                                                                                                                                                                                                    QGEWGTICDDGWDSYDAAVACKQLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVW
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  IGRHNCRHSEDAGVIC
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                                                                                                        ICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGKGPIHVDNVKCTGNERSLADCIKQD
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41 1149 M130 ANTIC
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Pred. No. 2.40e-208;
73; Mismatches 172;
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                         Q07900 PRELIMINARY: PRT; 1156 AA. Q07900; Q07900; Q1-NOV-1996 (TrEMBLrel. 01, Created) Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update) Q1-NOV-1996 (TrEMBLrel. 12, Last annotation update) M130 ANTIGEN, CYTOPLASMIC VARIANT 2 PRECURSOR. Homo sapiens (Human). Homo sapiens (Human).
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Q1-NOV-1999 (TrEMBLrel 12, Last annotation up
M130 ANTIGEN, CYTOPLASMIC VARIANT 1 PRECURSOR,
Homo sapiens (Human).
                Eutheria; Primates;
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EMBL; 222969; CAA80542.1; -.
PFAM; PF00530; SRCR; 9.
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MEDLINE; 93380506.
LAW S.A., MICKLEM K.J.,
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les 171; Conservative
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                                                                                                                                                                                                                                                                      VCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWLFLSSCNGNETSLWDCKNWQ 451
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41 1151 M130 ANTIGEN, CYTOP
1151 AA; 124820 MW; A72EDD2F CRC32;
                Catarrhini;
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73; M
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              Hominidae;
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Eur. J. Immunol. 23:2320-2325(1993).
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MEDLINE; 93380506.
LAW S.A., MICKLEM K.J.,
MASON D.Y.;
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Local Similarity 39.2%;
les 171; Conservative
                                                                              VCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWLFLSSCNGNETSLWDCKNWQ
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IGRHNCRHSEDAGVIC
                           WGGLTCDHYEEAKITC
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1156 AA;
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1156 M130 ANTIGEN,
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Pred. No. 2.40e-208;
73; Mismatches 172;
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M130 ANTIGEN, CYTOPLASMIC VARIANT
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US-09-147-947-6-02.rag Ma 3 may be accordable

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

dďī protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 13 10:22:30 2000; MasPar time 5.73 Seconds 301.681 Million cell updates/sec

Tabular output not generated.

Title: >US-09-147-947-6

Description: Perfect Score: (40-112) from US09147947A.pep (2 of 6) 611

Sequence:

Scoring table:

CPAGEPWVSVTDFGAPCLRW.....RPWCFYGDARGKVDWGYCDC 73

PAM 150 Gap 11

Searched

Post-processing: Minimum Match 0% Listing first 45 summaries

188963 seqs, 23686106 residues

Database:

a-geneseq35

Statistics: Mean 27.866; Variance 105.747; scale 0.264

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Best Local 9
W83361 standard; Protein; 875 AA.
W83361;
17-FEB-1999 (first entry)
Human neurotrypsin; tumour inhibition; neurological disease;
Human; neurotrypsin; tumour inhibition; neurological disease;
lung disease; gene therapy; drug development; stroke; brain injury;
neurologeneration; neuroinflammatory disease; multiple sclerosis;
epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                    New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Claim !; Page 61-65; 69pp; Japanese.

The present sequence is a serine protease designated BSSP-3, which is isolated from human brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs.
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W99087;
13-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            serine protease in 
Sequence 822 AA;
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N-PSDB; X19024
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24-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents human neurotrypsin. Neurotrypsin proteins and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or rettina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration, euroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to norease survival of damaged neurons (e.g. in cases of hypoxia, or section) and to stimulate regeneration and/or asschaemia, nerve transection) and to stimulate regeneration and/or restoration or neoangiogenesis; (v) to treat or prevent apoptosis (or other causes of cell death) in the nervous system; (vii) to regenerate brain and/or nervous tissue; (viii) to treat pain; (ix) to improve brain performance, including learning and memory; (x) to treat or prevent a wide range of psychiatric disorders; and (xi) to treat brain or lung wide range of psychiatric disorders; and (xi) to treat brain or lung and memory; (x) to 
The present sequence represents mouse neurotrypsin. Neurotrypsin p and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or retina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurodegeneration; neu epilepsy; hypoxia; isc emphysema; bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchitis).
                                                                                                                               gene therapy and in drug development Claim 1; Page 29-32; 50pp; English.
                                                                                                                                                                               New human and murine neurotrypsin - used, e.g. for inhibiting tumours, treatment of neurological or lung disease, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W83362 standard; Protein; 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumours, treatment of neurological or lung gene therapy and in drug development Claim 1: Page 20-24; 50pp; English.
                                                                                                                                                                                                                                           N-PSDB; V72590
                                                                                                                                                                                                                                                                   Sonderegger P;
WPI; 99-009438/01.
                                                                                                                                                                                                                                                                                                                                            24-APR-1998; IB0625.
26-APR-1997; CH-000966.
                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                          WO9849322-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse neurotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W83362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V72589.
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26-APR-1997; CH-000966.
(SOND/) SONDEREGGER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            injury associated with protease expression (specifically emphysema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human and murine neurotrypsin - used, e.g. for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09849322
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                                                                                                                                                                                                                                                                                                                      (SOND/) SONDEREGGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.0%; es 73; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus.

    e; neurotrypsin; tumour inhibition; neurological disease;
disease; gene therapy; drug development; stroke; brain in
odegeneration; neuroinflammatory disease; multiple scleros

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPAGEPWVSVTDFGAPCLRWAEVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DARGKVDWGYCDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DARGKVDWGYCDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99-009438/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ischaemia; nerve transection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                                                                                                                                                                                                                                         ים
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 611; DB 1; Le
Pred. No. 1.69e-54;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease,
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                                                                                                                                                                                  including
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 injury;
                             damage
on the
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Matches
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Best Local
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                                                                                                                               W52815 standa
W52815;
07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1999.
24-JUL-1998;
24-JUL-1997;
                                                Tissue plasminogen activator variant 2. tPA; fibrin-stimulated; clot; treatment; fibrin deposition; adhesion formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) t increase survival of damaged neurons, (e.g. in cases of hypoxia, ischaemia, nerve transection) and to stimulate regeneration and/or restoration of synapses; (v) to treat or prevent retinal disorders (e.g. degeneration or neoangiogenesis); (vi) to prevent apoptosis (or other causes of cell death) in the nervous system; (vii) to regenerate brain and/or nervous tissue; (viii) to treat pain; (ix) to improve brain performance, including learning and memory; (x) to treat or prevent a wide range of psychiatric disorders; and (xi) to treat brain or lung
                         Synthetic
                                             fibrin deposition; adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Example 1; Page 51-54; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W99088 standard; Protein; W99088;
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Sequence 761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; X19027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsuruoka N, Yamaguchi N, Yamashiro WPI; 99-142942/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease; BSSP-3; brain tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse serine protease BSSP-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-1997; JP-213969.
(SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                100
                                                                                                                                                                                                                                                                                                                                                      145
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                                                                                                                                                                                                                                                                                                                                                                                                        40
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sapiens
                                                                                                                                                                                                                                                                                                                            NAQGKVDWGYCDC
                                                                                                                                                                                                                                                                                                                                                                                                   NAQGKVDWGYCDC
                                                                                                                                                                                  .5 standard;
                                                                                                                                                                                                                                                                                                DARGKVDWGYCDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGESWGNATNLGVPCLHWDEVPPFLERSPPASWAELRGQPHNFCRSPDGSGRPWCFYR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.0%;
larity 78.1%;
Conservative
                                                                                                                                  (first entry)
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                                                                                                                                                                                  protein; 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 507; DB 1; Le
Pred. No. 4.16e-43;
9; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 507; DB 1; Le
Pred. No. 4.16e-43;
9; Mismatches 7;
                                                                                                                                                                                    A
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                                                                               vascular disease;
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R 03-OCT-1991; US-770510.

R 03-OCT-1993; US-088451.

PR 07-JAN-1994; US-179059.

PR 14-APR-1995; US-622891.

PR 19-OCT-1996; US-622891.

PR 17-OCT-1996; US-733353.

PA (GETH) GENENTECH INC.

PI Anderson S, Bennett WF, Botstein D, Higgins DL,

PI Anderson S, Bennett WF, Botstein D, Higgins DL,

PI Paoni NF, Zoller MJ;

PI Paoni NF, Zoller MJ;

PR WPI; 98-129803/12.

PT Treatment of vascular conditions or disease - using tissue

PT plasminogen activator variant having amino acid substitutions in

PT plasminogen activator variant having amino acid substitutions in
RESULT
ID WS
AC WS
DT 07
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Best Local S
Matches 2
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Disulfide_bond
Modified_site
                            LT 6
W52814
                                                                                                                                                                                                                                                                                                 protease domain to increase fibrin specificity
Claim 5; Page -; 3lpp; English.
Variants W52814-W52817 containing two or more functional regions were created from tissue plasminogen activator (tPA)(W52813). The t-PA variants have a higher fibrin-stimulated activity than fibrinogen-stimulated activity so they will act preferentially at the site of a clot and not systemically. They can be used for treating vascular diseases and conditions or to prevent fibrin deposition or adhesion formation or reformation.
 W52814;
07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide_bond
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Disulfide_bond
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                     Note: This sequence is not given in the specification from the wildtype t-PA sequence (W52813) disclosed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide_bond Cleavage_site
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                                                                                   106
                                                                                                                                                                       105
                                                                                                                164 TWEYCD 169
                                                                                                                                            48
                                                                                                                                                         SLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHYLKNR-RL 163
                                                                                   DWGYCD
                                                                                                                                            SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
                          standard;
                                                                                                                                                                                                   Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-383608.
US-240856.
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240856
                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-
114. .156
145. .169
177. .308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93. 174
/note= "Kringle-2 domain"
177. 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "finger domain"
                            protein;
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e= "contains the growth factor domain"
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                             483
                                                                                                                                                                                                  Score 195;
Pred. No. 5.
15; Mismatc
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tches 22;
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02-SEP-1988; US-240856.
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06-JUL-1993; US-088451.
07-JAN-1994; US-179059.
14-APR-1995; US-422736.
29-MAR-1996; US-733353.
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                                                                                                                                                                       Treatment of vascular conditions or disease - using tissue plasminogen activator variant having amino acid substitutions in protease domain to increase fibrin specificity
Claim 4; Page -; 31pp; English.
Variants W52814-W52817 containing two or more functional regions were created from tissue plasminogen activator (tPA)(W52813). The t-PA variants have a higher fibrin-stimulated activity than fibrinogen-stimulated activity so they will act preferentially at the site of a clot and not systemically. They can be used for treating vascular diseases and conditions or to prevent fibrin deposition or adhesion formation or reformation.

Note: This sequence is not given in the specification but was created from twildtype t-PA sequence (W52813) disclosed by the inventors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5714145-A.
03-FEB-1998.
02-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                            Anderson S, Bennett WF, Paoni NF, Zoller MJ; WPI; 98-129803/12.
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                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                            208
                                                                                149
  106 DWGYCD 111
                                                      48
                                                                     SLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHYLKNR-RL 207
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                            TWEYCD 213
                                                      SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
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26; Conse
                                                                                                          larity 39.4%;
Conservative
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157. .199
188. .212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "serine protease domain"
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15; M
                                                                                                          No. 5.34e-10;
Mismatches 22;
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                                                                                                                                   Length 483;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
Goeddel DV, Leung DWH, Rice
WPI; 98-239153/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W54151;
20-JUL-1998
       Disulfide_bond
                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                    Tissue plasminogen activator.

tPA; fibrin-stimulated; clot; treatmen
fibrin deposition; adhesion formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       W52813;
07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W52813 standard; protein; 527
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Mutant tissue plasminogen activator proteins (W54147-W54158) are created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-1991; US-728456.
26-JAN-1993; US-008940.
01-APR-1994; US-221660.
13-FEB-1995; US-389615.
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Amino acid substitution; t-PA; vascular disorder; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W54151 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibrin deposition; adhesion formation.
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26; Conse
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Location/Qualifiers
6. .36
34. .43
51. .62
56. .75
75. .84
92. .173
113. .155
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Pred. No. 5.
15; Mismatc
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24-JUL-1989; US-383608.
02-SEP-1988; US-240856.
03-OCT-1991; US-770510.
06-JUL-1993; US-088451.
07-JAN-1994; US-179059.
14-APR-1995; US-422736.
29-MAR-1996; US-622891.
17-OCT-1996; US-733353.
                                                                                                                                                                                                                                                                                                   Treatment of vascular conditions or disease - using tissue plasminogen activator variant having amino acid substitutions in protease domain to increase fibrin specificity Disclosure, Fig 1; 31pp; English.

The Tissue plasminogen activator (tPA) was used to create variants (W52814-W52817) containing two or more functional regions. The t-PA variants have a higher fibrin-stimulated activity than fibrinogen-stimulated activity so they will act preferentially at the site of a clot and not systemically. They can be used for treating vascular diseases and conditions or to prevent fibrin deposition or adhesion formertion or reference or reference.
                                  20-JUL-1998 (first entry)
t-PA mutant (S127C; Y143H, C173R)
Amino acid substitution; t-PA; vascular disorder; prevention;
                                                           W54150 standard; protein; 527
W54150;
20-JUL-1998 (first entry)
          fibrin deposition; adhesion formation. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 98-129803/12.
Treatment of vascular conditions or disease
                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC.
Anderson S, Bennett WF,
Paoni NF, Zoller MJ;
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                                                                                                                                    106
                                                                                                                                                            252
                                                                                                                                                                                                           193
                                                                                                                                                                                  48
                                                                                                                                                                                               SLTESGASCLPWNSMILIGKYYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHYLKNR-RL 251
                                                                                                                                    DWGYCD
                                                                                                                                                           TWEYCD 257
                                                                                                                                                                                   SVIDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .fide_bond
                                                                                                                                                                                                                                 similarity 39.4%;
26; Conservative
                                                                                                                                                                                                                                                                                  formation or reformation. 527 AA;
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201. .2
232. .2
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264. .!
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51. .91
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180
184
Location/Qualifiers
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180. .:
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e= "contains the growth
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.384
.484
.457
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.527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N-glycosylation'
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Botstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Kringle-1
                                                                                                                                                                                                                                 Score 195; DB 1; Let Pred. No. 5.34e-10; 15; Mismatches 22;
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Query Match
Best Local S
Matches 2
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11-JUL-1991; US-728456.
26-JAN-1993; US-008940.
01-APR-1994; US-221660.
13-FEB-1995; US-389615.
                                                                                                                                                                                                                                                                                                                                                                                                      Mutant tissue plasminogen activator proteins - useful for treating vascular disorders, preventing tissue adhesion(s), etc. Claim 6; Page -; 24pp; English.

Mutant tissue plasminogen activator proteins (W54147-W54158) are created by single or multiple amino acid substitutions. Compositions containing the t-PA variant are used for treating vascular disorders, for preventing fibrin deposition or for preventing adhesion formation or reformation. Note: This sequence is not given in the specification but was created sequence 527 AA;
   US5736135-A
07-APR-1998
                                 misc_difference
                                                                                                                      Domain
                                                                                                                                                               Synthetic.
                                                                                                                                                                                 20-JUL-1998 (first entry)
t-PA mutant (K159R).
Amino acid substitution; t-PA; vascular disorder; prevention;
                                                                                                                                                                                                                    W54158 standard; protein; 527 AA. W54158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC. Goeddel DV, Leung DWH, Rice GC; WPI; 98-239153/21.
                                                                           Domain
                                                                                                 Domain
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Local Similarity 39.4%;
les 26; Conservative
                                                                                                                                                                                                                                                                                                                   SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
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                                                                                                                                                                                                                                                                                                                                       SLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHYLKNR-RL 251
                                                                                                                                                                         deposition; adhesion formation
                                 /note=
159
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127
                                                     780. .261
/note= "Kringle-2 domain"
                                                                                    92. .17
/note=
                                                                                                                     /note= "Finger domain"
45. .91
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180. .2
/note=
264. .
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45. .91
                                                                                                                                                   Location/Qualifiers
                     /note= "K changed from wt to R in mutant"
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                                                                                                          /note= "Growth factor domain"
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                                            "Serine protease domain"
                                                                                     "Kringle-1 domain"
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Pred. No. 5.:
15; Mismatch
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5.34e-10;
tches 22;
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Disulfide_bond
Modified_site
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11-JUL-1991;
26-JAN-1993;
26-JAPR-1994;
13-FEB-1995;
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WY 11
WY 21
WY 22

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Mutant tissue plasminogen activator proteins (W54147-W54158) are created by single or multiple amino acid substitutions. Compositions containing the t-PA variant are used for treating vascular disorders, for preventing fibrin deposition or for preventing adhesion formation or reformation. Note: This sequence is not given in the specification but was created from the wild type by the indexer.

Sequence 527 AA;
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                                                                                                                                                                                                                                                                                                                                 Disulfide_bond
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Local Similarity 39.4%;
hes 26; Conservative
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US-728456.

US-008940.

US-221660.

US-389615.
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180. .2
                                                                                                                                                                                                                                                                                                                                    441.
474.
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315
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201. .243
232. .256
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277
                                                                 /note=
                                                                                                                                                                                              /note= "finger domain"
51. 91
/note= "contains the g
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hte= "Kringle-l
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                                                                                                    .261
                                      .527
                                                                 "Kringle-2 domain
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"serine proteases domain"
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Pred.
15; M
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. No. 5.34e-10;
Mismatches 22;
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Best Local
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07-JAN-1994; US-179059.
14-APR-1995; US-422736.
29-MAR-1996; US-622891.
17-OCT-1996; US-733353.
  Goeddel
WPI; 98
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02-SEP-1988;
02-SEP-1989;
24-JUL-1988;
02-SEP-1998;
03-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                    T 12
W54157 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page -; 31pp; English.

Variants W52814-W52817 containing two or more functional regions were reated from tissue plasminogen activator (tPA)(W52813). The t-PA ariants have a higher fibrin-stimulated activity than ribrinogen-stimulated activity so they will act preferentially at the site of a clot and not systemically. They can be used for treating vascular diseases and conditions or to prevent fibrin deposition or adhesion formation or reformation.

Note: This sequence is not given in the specification but was created from the wildtype t-PA sequence (W52813) disclosed by the inventors. Sequence 527 AA;
                                                                                                  US5736135-A.
                                                                                                                                     misc_difference
                                                                                                                                                             Domain
                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                       20-JUL-1998 (first entry)
t-PA mutant (N142S).
Amino acid substitution; t-PA; vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease domain to increase
Claim 7; Page -; 31pp; Engli
                                     01-APR-1994; US-221660.
13-FEB-1995; US-389615.
                                                          13-FEB-1995; 389615.
11-JUL-1991; US-728456.
26-JAN-1993; US-008940.
                                                                                                                                                                                                           Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of vascular conditions or disease - using tissue plasminogen activator variant having amino acid substitutions
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Anderson S, Bennett WF, Botstein
Papani NF, Zoller MJ;
WPI: 98-129803/12.
                          (GETH )
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del DV, Leung DWH,
98-239153/21.
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                                                                                                                                                                                                                                                                                             deposition; adhesion
                GENENTECH
DV, Leung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 31.9%;
Similarity 39.4%;
26; Conservative
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US-240856.
US-770510.
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142
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e= "Kringle-2 domain"
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                                                                                                                                                                                                                                             "Finger domain"
                Rice
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W54156;
20-JUL-1998
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26-JAN-1993;
01-APR-1994;
13-FEB-1995;
                                               Mutant tissue plasminogen activator proteins - useful for treating vascular disorders, preventing tissue adhesion(s), etc. Claim 2; Page -; 24pp; English.

Mutant tissue plasminogen activator proteins (W54147-W54158) are created by single or multiple amino acid substitutions. Compositions containing the t-PA variant are used for treating vascular disorders, for preventing fibrin deposition or for preventing adhesion formation or reformation. Note: This sequence is not given in the specification but was created sequence 527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant tissue plasminogen activator proteins - useful for trea vascular disorders, preventing tissue adhesion(s), etc. Claim 2; Page -; 24pp; English.

Mutant tissue plasminogen activator proteins (W54147-W54158) a by single or multiple amino acid substitutions. Compositions the t-PA variant are used for treating vascular disorders, for fibrin deposition or for preventing adhesion formation or refo Note: This sequence is not given in the specification but was from the wild type by the indexer.
                                                                                                                                                                    (GETH ) GENENTECH INC. Goeddel DV, Leung DWH, WPI; 98-239153/21.
                                                                                                                                                                                                                                                                                                      misc_difference
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Key
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07-APR-1998.
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  Similarity
26; Conser
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US-008940.
US-221660.
US-389615.
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larity 39.4%;
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Pred. No. 5.34e-10;
15; Mismatches 22;
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Mutant tissue plasminogen activator proteins (W54147-W54158) are created by single or multiple amino acid substitutions. Compositions containing the t-PA variant are used for treating vascular disorders, for preventing fibrin deposition or for preventing adhesion formation or reformation.

Note: This sequence is not given in the specification but was created from the wild type by the indexer.
                                 t-PA mutant (Y156D)
Amino acid substitution; t-PA; vascula
fibrin deposition; adhesion formation.
                                                                       W54155;
20-JUL-1998 (first entry)
                                                                                               W54155 standard; protein; 527
                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC. Goeddel DV, Leung DWH, Rice GC; WPI; 98-239153/21.
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misc_difference 115
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Amino acid substitution; t-F
fibrin deposition; adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W54148 standard; protein; 527 W54148;
                         Synthetic.
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13-FEB-1995; US-389615.
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larity 39.4%;
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/note= "Growth factor domain"
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ion formation.
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Mutant tissue plasminogen activator proteins (W54147-W54158) are created by single or multiple amino acid substitutions. Compositions containing the t-PA variant are used for treating vascular disorders, for preventing fibrin deposition or for preventing adhesion formation or reformation. Note: This sequence is not given in the specification but was created sequence 527 AA;
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106 DWGYCD 111
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                         TWEYCD 257
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                                                                          SLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHYLKNR-RL 251
                                                                                                h 31.9%;
Similarity 39.4%;
26; Conservative
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protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:22:56 2000; MasPar time 4.22 Seconds 224.268 Million cell updates/sec

Title: .

Description: Perfect Score: >US-09-147-947-6 (40-112) from US09147947A.pep (2 of 6) 611

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Scoring table: PAM 150 Gap 11 Sequence:

131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

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Statistics: Mean 26.490; Variance 105.747; scale 0.251

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	29.0 339 2 US-08-866- Sequence 6, Applicatio 4.30e- 29.0 339 3 PCT-US95-0 Sequence 6, Applicatio 4.30e-	29.0 339 2 US-08-612- Sequence 6, Applicatio 4.30e- 29.0 339 2 US-08-866- Sequence 6, Applicatio 4.30e- 29.0 339 3 PCT-US95-0 Sequence 6, Applicatio 4.30e-	29.0 339 1 US-08-452- Sequence 6, Applicatio 4.30e- 29.0 339 1 US-08-248- Sequence 6, Applicatio 4.30e- 29.0 339 2 US-08-6612- Sequence 6, Applicatio 4.30e- 29.0 339 2 US-08-866- Sequence 6, Applicatio 4.30e- 29.0 339 3 PCT-US95-0 Sequence 6, Applicatio 4.30e-	29.0 339 1 US-08-326- sequence 6, Applicatio 4.30e- 29.0 339 1 US-08-452- sequence 6, Applicatio 4.30e- 29.0 339 1 US-08-248- sequence 6, Applicatio 4.30e- 29.0 339 2 US-08-6612- sequence 6, Applicatio 4.30e- 29.0 339 2 US-08-866- sequence 6, Applicatio 4.30e- 29.0 339 3 PCT-US95-0 sequence 6, Applicatio 4.30e-	29.0 250 2 US-08-612- Sequence 33, Applicati 4.30e- 29.0 339 1 US-08-726- Sequence 6, Applicatio 4.30e- 29.0 339 1 US-08-452- Sequence 6, Applicatio 4.30e- 29.0 339 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4.30e- 29.0 339 1 US-08-248- Sequence 6, Applicati 4.30e- 29.0 339 2 US-08-66- Sequence 6, Applicati 4.30e- 29.0 339 2 US-08-66- Sequence 6, Applicati 4.30e- 29.0 339 2 US-08-66- Sequence 6, Applicati 4.30e- 29.0 339 3 PCT-US95-0 Sequence 6, Applicati 4.30e-	29.3 527 1 US-07-609 Sequence 16, Applicatio 2.77e- 29.3 527 2 US-08-811- Sequence 39, Applicatio 2.77e- 29.3 527 2 US-08-811- Sequence 39, Applicatio 2.77e- 29.3 542 4 5200340-6 Patent No. 5200340. 2.77e- 29.3 562 4 5200340-2 Patent No. 5200340. 2.77e- 29.3 562 4 5204676-5 Patent No. 5244676. 2.77e- 29.3 562 4 5244676-5 Patent No. 5244676. 2.77e- 29.3 562 2 US-08-811- Sequence 38, Applicati 2.77e- 29.3 562 2 US-08-81- Sequence 38, Applicati 2.77e- 29.3 562 2 US-08-883- Sequence 21, Applicati 2.77e- 29.3 562 2 US-08-612- Sequence 21, Applicati 4.30e- 29.0 250 2 US-08-612- Sequence 6, Applicati 4.30e- 29.0 339 1 US-08-452- Sequence 6, Applicati 4.30e- 29.0 339 1 US-08-248- Sequence 6, Applicati 4.30e- 29.0 339 2 US-08-66- Sequence 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ALIGNMENTS

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TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 946 amino acids TYPE: amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE 946 AA; 105892 MW; 4559778 CN;	NAME: Brown, Scott A REGISTRATION NUMBER: 32,724 REFERENCE/DOCKET NUMBER: GI5234A TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224	LICATION DATA: ON NUMBER: PCT/US95/0849 TE: ATION: ENT INFORMATION:	COMPUTER READABLE FORM: COMPUTER READABLE FORM: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25	A HOOOESE	1 CT-US95-0 xxxxx equence 1 sequence

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Query Match
Best Local Similarity
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ID 5520913-1
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Matches 26; Conservative
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                                                                                                                                                       Sequence 4, Application US/08427640
                                                                                                                                                                                                                                        US-08-427-640-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                Sequence 4, Application US/08427640 Patent No. 5658788
                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                              106 DWGYCD 111
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                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/
FILING DATE: 06-JUL-1993
PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: E11 L111y and Company
STREET: L111y Corporate Center
CITY: Indianapolis
                                                      APPLICANT: Berg et al.
TITLE OF INVENTION: CO
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 35
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 770,510
FILING DATE: 03-OCT-1991
APPLICATION NUMBER: 384,608
FILING DATE: 24-JUL-1989
APPLICATION NUMBER: 240,856
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                                                                                                                                                                                                                                          STANDARD;
                                                                      Compounds and Methods for Treatment of Thromboembolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/88,451
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Pred. No. 5.92e-09;
16; Mismatches 22;
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13; Mismatches 23;
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Best Local
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TOPOLOGY: linear
MOLECULE TYPE: protein
MOLECULE TYPE: protein
MW; 642605 CN;
MG: 2.
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APPLICATION NUMBER: 07/689,410

FILING DATE: 22 APRLI 1991

INFORMATION FOR SEQ ID NO: 4:
                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                       APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                  STALL
COUNTRY: CC
COUNTRY: CC
COUNTRY: CC
             APPLICATION NUMBER: US/08/811,949 FILING DATE: 05-MAR-1997
                                                                                                                                                                   STREET: 1755 S. CITY: ARLINGTON
  CLASSIFICATION:
                                                                                                                                                                                              ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/427,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
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25; Conser
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5840533
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                                                                                                                                                                                   1755 S.
                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                        NIWA, MINEO
SAITO, YOSHIMASA
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                                                                                                                                                                                JEFFERSON DAVIS HIGHWAY, SUITE
                                                                                                                                                                                                           SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 180;
Pred. No. 2.
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335 22;
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Patent No. 5840533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 DWGYCD 111
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es 25; Conser
                ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-220
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                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUS ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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37.9%;
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Pred. No. 2.77e-08;
15; Mismatches 23;
                                                                            18-966-0
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Best Local S
Matches 2
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                                                                                                                                                        TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 TWEYCD 85
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Local Similarity 37.9%;
les 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION UNMBER: 24,618
REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
MOLECULE TYPE: protein JENCE 355 AA; 39550 MW; 638607 CN;
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                                                                                                                           SEQUENCE CHARACTERISTICS:
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APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NIWA, MINEO APPLICANT: SAITO, YOSH
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                                                                      TYPE: amino acid
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ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
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                                                                                                                                                  TELEPHONE: 703-413-2220
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CITY: ARLINGTON
                                                    TOPOLOGY:
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                                                                                                 LENGTH:
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SASAKI, HITOSHI
HAYASHI, MASAKO
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Pred. No. 2.77e-08;
15; Mismatches 23;
                                                                                                                                                        59:
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Query Match
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Best Local :
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                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-137-116-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08137116 Patent No. 5500411
                                                                          equence 1, Application US/08137116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 DWGYCD 111
                                                        TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 37.9%, nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 TWEYCD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THENT NO. SOUTTENT ON:
                                                                                                                                              APPLICATION NUMBER: DE 41 12 398
FILING DATE: 16 April 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 41 23 845
FILING DATE: 18 July 1991
                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP92/00851
FILING DATE: 15 April 1992
PRIOR APPLICATION DATA:
                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                  TOPOLOGY: 1:
NCE 355 AA;
                                                                                                                                                                                                                                        FILING DATE: JUCCLASSIFICATION:
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: June 30, 1994
                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                10022
                                                                                                                                                                                                                                                                                                                                                           New York
                                      amino acids
                                                                                                                                                                                                                                                                                                                                                 New York
                                                 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                     805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martin,
                                                                                                                                                                                                                                                                                                  IBM PS/2
                   39589 MW; 639067 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.3%;
                                                                                                                                                                                                                                                                                                          Diskette, 5.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
 29.38;
                                                                                                                           No. 5500411man D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ulrich
Reinhard
                                                                                                                                                                                                                                                                                         PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                           ADMINISTRATION OF THROMBOLYTICALLY ACTIVE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                              METHOD FOR TREATING THROMBOEMBOLIC CONDITIONS BY INHIBITING REOCCLUSION VIA THE USE OF MULTIPLE BOLUS
                                                                                                                                                                                                                                                            US/08/137,116
Score 179;
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Pred. No. 2.77e-08;
15; Mismatches 23;
                                                                                                          BOER 1026
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                                                                                                                                                                                                                                                                                                           inch, 360 kb storage
DB 1;
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Length 355;
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ID 5223256-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: STERN, ANNE:KOHNERT, ULRICH;RUDOLPH, RAINER;
FISCHER, STEPHAN;MARTIN, ULRICH
TITLE OF INVENTION: THROMBOLYTICALLY ACTIVE NON-GLYCOSYLATED
                                                                                                                                                                                                                     Sequence 47, Application U9/08811949
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                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                Sequence 47,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 29.3%;
Local Similarity 37.9%;
                                                                                                           APPLICANT: NIWA, MINEO
APPLICANT: SARITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 80 TWEYCD 85
                                                                                                                                                                                                                                                                                                                                                                                                        21 SLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNR-RL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
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                                                             APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CURRENT APPLICATION NUMBER: US
APPLICATION NUMBER: US
STREET: 1/JU
STREET: 1/JU
CITY: ARLINGTON
CTATE: VA
                             ADDRESSEE: OBLOI
ADDRESSEE: P.C.
STREET: 1755 S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 AA; 42894 MW; 827068 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                               Application US/08811949
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                                                   OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-1990
                                                                                                                                                                                                                                                                                              STANDARD;
                              JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/07/585,129
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15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 179; DB 4;
Pred. No. 2.77e-08;
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15; Mismatches 23;
                                                                                                                                                                                                                                                                                            PRT;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY:

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RESULT
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Best Local Similarity
Matches 25; Conser
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                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .80 TWEYCD 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 SLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNR-RL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ.ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                        GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/
FILING DATE: 25-MARCH-1994
                                                                                                                                                                                              APPLICANT: Fischer, Stephan
TITLE OF INVENTION: METHOD FOR TREATING THROMBOEMBOLIC CONDITIONS
TITLE OF INVENTION: BY INHIBITING REOCCLUSION VIA THE USE OF
TITLE OF INVENTION: MULTIPLE BOLUS ADMINISTRATION OF
TITLE OF INVENTION: THROMBOLYTICALLY ACTIVE PROTEINS
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
UENCE 355 AA; 39543 MW; 638851 CN;
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                     ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                             STREET: 805 Thir
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
                                                  COMPUTER: IBM PS,
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                         10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%;
ilarity 37.9%;
Conservative
                                                                                                                                                                                                                                                                                                                  Application US/08217616
                                                                                                                                                          805 Third Avenue
                                                                                                                   USA
                                                                                                                                                                                                                                                                              Martin, Ulrich
                                                                 IBM PS/2
                                                                            Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                   PC-DOS
             US/08/217,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 179; DB 2; Le
Pred. No. 2.77e-08;
15; Mismatches 23;
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                                                                             inch,
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                                                                             MB storage
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 DWGYCD 111
                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
        ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.3%;
Local Similarity 37.9%;
les 25; Conservative
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TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 TWEYCD 85
                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5690931man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                       APPLICATION NUMBER: US/08/811,949 FILING DATE: 05-MAR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                            STREET: 1755 S. CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                         ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1026.1
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                                                                                                                                                                                              22202
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SAITO, YOSHIMASA
SASAKI, HITOSHI
HAYASHI, MASAKO
                                                                                                                                                                                                         USA
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Pred. No. 2.77e-08;
15; Mismatches 23;
                                             18-966-0
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Best Local (
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                       Local Similarity hes 25; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 29.3%;
Local Similarity 37.9%;
Les 25; Conservative
                                                                                                                                                                                                                                                    TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 TWEYCD 85
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                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPEFFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 25-MARCH-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acid
                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                             TYPE: a
                                                                                                                                                                          TYPE: amino acids TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                             NAME: Hanson, No. 5510330man REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10022
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355 AA; 39517 MW; 639267 CN;
                                                                                                                                                         355 AA; 39589 MW; 639067 CN;
                                                                           29.3%;
ilarity 37.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fischer, Stephan
PENTION: COMBINATIONS OF THROMBOLYTICALLY ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martin, Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Pred. No. 2.77e-08;
15; Mismatches 23;
                                                                             Score 179; DB 1; L
Pred. No. 2.77e-08;
15; Mismatches 23;
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RESULT
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Best Local Similarity
Matches 25; Conser
US-08-427-640-2
                                                                                                                                                                                                                                                     SEQUENCE
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                                                            106 DWGYCD 111
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                                                                                                                                                      21 SLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNR-RL 79
                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 TWEYCD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25
                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acid
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                           SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                   TOPOLOGY: linear
ICE 355 AA; 39589 MW; 639067 CN;
                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/
FILING DATE: 25-MARCH-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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llarity 37.9%;
Conservative
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805 Third Avenue
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stephan
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                                                                                                                                                                                     Pred. No. 2.77e-
15; Mismatches
                                                                                                                                                                                                      Score 179; DB 1;
Pred. No. 2.77e-08;
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PRT;
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Sequence 2, Application US/08427640

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Best Local 9
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                                                                                                                                                         Sequence 6, Application US/08427640 Patent No. 5658788
                                                                                                                                  Patent No. 5658788
GENERAL INFORMATION:
APPLICANT: Berg e
                                                                                                                                                                                                                                                                                                             106 DWGYCD 111
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                                                                                                                                                                                                                                                                                                                                                                                                       Match 29.3%;
Local Similarity 37.9%;
les 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    80 TWEYCD 85
                                                                                                                                                                                                                                                                                                                                                                      48 SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/689,410
APPLICATION NUMBER: 07/689,410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: MICROSOFT WORD CURRENT APPLICATION DATA: APPLICATION NUMBER: US/O
                                                                                                          APPLICANT: Berg et al.
TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Discounds OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein JENCE 355 AA; 39589 MW; 639067 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                CORRESPONDENCE ADDRESS:
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                                                CITY: Indianapolis STATE: IN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Macintosh
OPERATING SYSTEM: M
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                                        COUNTRY:
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                                                                         E: Eli Lilly and Company
Lilly Corporate Center
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Lilly Corporate Center
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                                        U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compounds and Methods for Treatment of Thromboembolic Disc
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Pred. No. 2.77e-08;
15; Mismatches 23;
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Best Local Similarity 37.9%;
Matches 25; Conservative
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MOLECULE TYPE: protein
SEQUENCE 355 AA; 39563 MW; 638774 CN;
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/689,410
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                       106 DWGYCD 111
                                                                                                                                 21 SLTESGASCLPWNSMILIGKVYTAQNGSAQALGLGKHNYCRNPDGDAKPWCHVLKNR-RL 79
                                                                                 80 TWEYCD 85
                                                                                                            48 SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DAPPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Macinto OPERATING SYSTEM:
                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                               Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                       Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                    DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            Macintosh
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                                                                                                                                                               Score 179; DB 1; Le
Pred. No. 2.77e-08;
15; Mismatches 23;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

h_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 13 10:22:03 2000; MasPar time 8.65 Seconds 398.104 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title: >US-09-147-947-6 (40-112) from US09147947A.pep (2 of 6) 611

Scoring table: PAM 150 Gap 11 .

Sequence: 1 CPAGEPWVSVTDFGAPCLRW......RPWCFYGDARGKVDWGYCDC 73

Searched:

142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 36.459; Variance 65.448; scale 0.557

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

· rt	Score	Query	Length 1	BB	ID		Pred. No.
W.	507	3	6	2	JC5759	brain-specific serine	.32e-
(Z)	207	ω.	4	μ	A47299	-related receptor	.02e-2
J	185	0	ш	٢	KFHU12	fa	
4	179	29.3	559	Н	A29941	en activ	.12e-1
5	179	9	Φ.	سر	UKHUT	lasminogen activa	.12e-1
6	175		\vdash	سا	A40332	rophage-stimulati	5e-
7	174	8	\vdash	Н	PLBO	3.4.21	.06e-
· œ	173	8	$\mathbf{\mu}$	۳	JC5061	macrophage-stimulatin	.65e-1
9	172	8	\vdash	μ	PLMS	plasmin (EC 3.4.21.7)	e-1
10	171	.8	0	2	S28941	oagulation factor	.04e-1
11	171	8	ဖ	μ	PATA	EC	.04e-1
12	169	.7	9	N	œ	tion factor	.83e-1
13	167	7.	O	ш		yaluronan-	.39e-1
14	165	7.	G	N	87	lasma	.78e-1
15	164	6,	ū	μ		<pre>-plasminogen acti</pre>	.98e-1
16	163	6	N	Н	JH0579	owth fa	
17	161	6.	₩,	Н	A47136	-stimula	.36e-1
18	161	26.4	Ν	۳	A35644	hepatocyte growth fac	.36e-1
19	161	5	2	۳	A60185		.36e-
20	161	6	\vdash	N	I46260	C 3.4.21	.36e-
21	159	σ,	-	٢	151283	hepatocyte growth fac	.07e-
22	. 157	5	4	μ	S00657	(a) (EC	.93e-
23	156	5	g	2	A40522	3.4.21.	.99e-

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N	N	N	w	ω	w	w	w	137	w	w	w	4	140	4	146	4	4	4	4	iπ	154	•
	20.6	۳	۲.		1.	۲.		۲.				2	22.9	ω.	ω.	ω.		4.	4.	4.	5	
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TBBO	S10511	UKBAY	A35827	TBHU	608	N056	E61545		UKPG	UKHU	JS0600	UKMS	014	1893	B61545	6154	Ξ	084	128	A46688	286	
3.4.21.	ombin (EC	nogen activa	3.4.21.	ombin (EC 3.4.2	lasminogen activa	-plasmi	lasmin (EC	(EC 3.	u-plasminogen activat	u-plasminogen activat	-plasminogen activa	u-plasminogen activat	C 3.4.2	<pre>-plasminogen act</pre>	lasmin (EC 3.4.	lasmin (EC 3.4.2	lasmin (EC 3.4.21.	smin (EC 3.4.21	growth 1	ס	apolipoprotein(a) (EC	
.41e-0	.36e-	.75e-0	.21e-0	.00e-0	.00e-0	.49e-0	.30e-0	.99e-1	.57e-1	.57e-1	.32e-1	.84e-1	Ļ	.22e-	.22e-1	.22e-	.45e-	Ŀ	.16e-1	.01e-	2e-1	

ALIGNMENTS

##molecule	#accession	#cross-refere			#title	#journal		#authors	REFERENCE	ACCESSIONS		DATE	ORGANISM	TITLE	ENTRY	RESULT 1	
##molecule_type mRNA	JC5759	#cross-references MUID:98008848	cysteine-rich motifs.	with a kringle-like structure and three scavenger receptor	Molecular cloning of a novel brain-specific serine protease	Biochem. Biophys. Res. Commun. (1997) 239:386-392	Tsujimura, A.; Yamaguchi, N.	Yamamura, Y.; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.;	JC5759	JC5759	17-Mar-1999	24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change	#formal_name Mus musculus #common_name house mouse	brain-specific serine proteinase (EC 3.4.21) - mouse	JC5759 #type complete		

KEYWORDS FEATURE 85-157 163-266 CLASSIFICATION ##residues 1.761 ##label YAM
##cross-referencés DDBJ:D89871
##experimental_source brain
##cxperimental_source brain
fFICATION #superfamily trypsin homology; scavenger receptor
cystecine-rich domain homology
RDS glycoprotein; hydrolase; serine proteinase

В 562,612,711 SUMMARY Query Match 83.0%; Best Local Similarity 78.1%; Matches 57; Conservative 513-516 517-755 93,521,569 166-266,273-372, 386-486 85 CGAGESWGNAINLGVPCLHWDEVPPELERSPPASWAELRGQPHNFCRSPDGSGRPWCFYR 144 #length 761 #domain furin binding #status predicted #label FRB\
#domain typsin homology #label TRY\
#binding_site carbohydrate (Asn) (covalent) #status
predicted\
#active_site His, Asp, Ser #status predicted
#th 761 #molecular-weight 84136 #checksum 5449 #domain kringle-like #status predicted #label KRI\ #domain scavenger receptor cysteine-rich domain homology #label SRC7\ #domain scavenger receptor cysteine-rich #status
predicted #label SRC\ Score 507; DB 2; Le Pred. No. 2.32e-88; 9; Mismatches 7; Length 761; Indels 0; 0;

밁 Ωy 145 NAQGKYDWGYCDC 157 40 CPAGEPWVSVTDFGAPCLRWAEVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYG 99

δÃ

100 DARGKVDWGYCDC

112

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658-666
225,340,477,544
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ccession A47299
                                                                                                       #accession
                                                                                                                      5'-flanking region.
#cross-references MUID:88007593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##experimental_source electric organ
##note sequence extracted from NCBI backbone (NCBIN:128724,
NCBIP:128726)
                                     ##cross-references
                                                             ##residues
                                                                        ##molecule_type DNA
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##residues
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26; Conser
                                                                                                                                                          Cool, D.E.; MacGillivray, R.T.A.

J. Biol. Chem. (1987) 262:13662-13673

Characterization of the human blood coagulation factor gene. Intron/exon gene organization and analysis of t
                                                                                                                                                                                                                                                                                                           coagulation factor XIIa (EC 3.4.21.38) precursor - human Hageman factor (activated) #formal_name Homo sapiens #common_name man 27.Nov.1985 #sequence_revision 30.Jun-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily Torpedo ror-related receptor; kringle homology;
protein kinase homology
ATP; glycoprotein; kringle; phosphotransferase; transmembrane
                                                                                                                                                                                                                                                                        A29411; A26814; A00930; A25191; A22248;
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larity 39.4%;
Conservative
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#region protein kinase ATP-binding motif\
#binding_site carbohydrate (Asn) (covalent) #status
                            1-615 ##label COO
:es GB:M17466; GB:J02807; NID:g180355; PIDN:AAB59490.1;
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                   PID:g180357
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Pred. No. 3.02e-23;
13; Mismatches 23;
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#pathway
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                                                                                                                                                                                                                                                                                                                                    #gene
                                                                                                                                                                                                                                                                                                                                                                                                  #authors Harris, R.J.; Ling, V.T.; Spellman, M.W.
#journal J. Biol. Chem. (1992) 267:5102-5107
#title O-linked fucose is present in the first epidermal growth
factor domain of factor XII but not protein C.
#cross-references MUID:92184750
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#title
                                                                                                                                                                                                                                                                      #map_position
#introns
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#journal J. Biol. Chem. (1983) 258:10924-10933
#title Amino acid sequence of human beta-factor XIIa.
#cross-references MUID:83291041
#accession A21037
                                                                                                                                                          #description
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#accession A22248
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##residues 354-362;373-615 ##label FUJ
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##cross-references GB.M31315;
WCF #00000
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                                                                  factor XIIa catalyzes the proteolytic activation of plasminogen, plasma prekallikrein, and coaqulation VII and IX; factor XII can catalyze the proteolyt. activation of prekallikrein blood coaqulation; fibrinolysis
                                                                                                                                                                                                                                                 5q34-5qter
19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McMullen, B.A., Fujikawa, K.
J. Biol. Chem. (1985) 260:5328-5341
Amino acid sequence of the heavy chain
XIIa (activated Hageman factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Que, B.G.; Davie, E.W.
Biochemistry (1986) 25:1525-1528
Characterization of a cDNA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Characterization of human blood coagulation factor XII cDNA. Prediction of the primary structure of factor XII and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brayer, G.D.; MacGillivray, R.T.A. J. Biol. Chem. (1985) 260:13666-13676
#superfamily coagulation; fibrinolysis
#superfamily coagulation factor XII; EGF homology;
fibronectin type I repeat homology; fibronectin typ
repeat homology; kringle homology; trypsin homology
                                                                                                                                                                                                     417/2; 463/1; 511/1; 560/3 factor XII, prekallikrein, and HMW kininogen bound to anionic surfaces
                                                                                                                                                                                                                                                                                                                                                                                  annotation; carbohydrate binding site
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NID:g182291; PIDN:AAA70225.1;
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NID:g180358; PIDN:AAA51986.1; PID:g180359
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                      fibronectin type
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                                                                                                                                     coagulation
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Best Local
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135-170
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217-295
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#cross-references MU #accession $48205
                                                                                                                                                                                                                   #title Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRNA and its expression during F9 teratocarcoinoma cell differentiation.
#cross-references MUID:88087303
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397-413,405-475,
436-439,500-569,
                                             #title
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83-198,200-209,
17-295,238-277,
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                                                                                                                           ##molecule_type mRNA
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                    Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D. Eur. J. Biochem. (1994) 224:863-871
Characterization of the murine plasma fibrinolytic system nces MUID:95010076
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                                                                                                                                                                                                                                                                                                                                                                                                                 t-plasminogen activator (EC 3.4.21.68) precursor - mouse #formal_name Mus musculus #common_name house mouse 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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kringle; plasma;
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predicted\
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#binding_site_carbohydrate (Thr) (covalent) #status
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#product coagulation factor XIIa, beta
experimental #label B12\
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#domain EGF homology #label EG1\
#domain fibronectin type I repeat homology #label 1F1\
#domain EGF homology #label EG2\
#domain EGF homology #label EG2\
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#product coagulation factor XIIa, alpha form #status experimental #label A12\
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Pred. No. 7.43e-19;
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                                                                                                                                                    REFERENCE
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88-105, 107-116,

124-205, 145-187,

176-200, 213-294,

234-276, 265-289,

297-288, 340-316,

348-417, 442-316,

474-490, 506-534
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Best Local
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#title
#accession A94
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213-294
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##residues 33-37,'X',39-40 ##label LIW
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##residues 309-316 ##label LI2
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##residues 33-37,'X',39-40 ##label
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Similarity 41.8%;
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             Ny, T.; Elgh, F.; Lund, B.
Proc. Natl. Acad. Sci. U.S.A. (1984) 81:5355-5359
The structure of the human tissue-type plasminogen
gene: correlation of intron and exon structures t
functional and structural domains.
The structural domains.
                                                                                                                                                                                                                                                                               t-plasminogen activator (EC 3.4.21.68) precursor
t-PA; tissue plasminogen activator
#formal_name Homo sapiens #common_name man
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14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change
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fibronectin type I repeat homology; kringle homology;
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A94004
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#domain EGF homology #label EGF\
#domain kringle homology #label KR1\
#domain kringle homology #label KR2\
#domain kringle homology #label KR2\
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predicted\
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    #product t-plasminogen activator chain A #status
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  predicted #label BCH\
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#domain propeptide #status predicted #label PRO\
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12; Mismatches
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Pred. No. 1.12e-17;
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#title Nucleotide sequence of the tissue-type plasminogen activator CDNA from human fetal lung cells.
#cross-references MUID:88262579
#cross-references S02125
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#cross-references_MUID:83115262
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itle Purification and characterization of tissue plasminogen activator secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.
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##cross-references GB:L00141
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                                            Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, Holmgren, E.; Josephson, S. Proc. Natl. Acad. Sci. U.S.A. (1983) 80:349-352
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Eriezner Degen, S.J.; Rajput, B.; Reich, E.
J. Biol. Chem. (1986) 261:6972-6985
                       Isolation of cDNA sequences coding
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plasminogen activator.
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source Detroit 562 cells; ATCC 138
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#title Cloning of cDNA coding for human tissue-type plasminogen
#cross-references MUID:86284200
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#journal EMBO J. (1986) 5:3525-3530
#title Involvement of finger domain and kringle 2 domain of tissue-type plasminogen activator in fibrin binding stimulation of activity by fibrin.
#cross-references MUID:87161761
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#journal J. Biol. Chem. (1986) 261:14214-14218
#cross-references MUID:87033611
#contents annotation; fibrin binding site
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##residues 1-562 ##label HAR
##cross-references GB:M15518; NID:g190031; PIDN:AAA60111.1; PID:g190032
##note parts of this sequence were confirmed by peptide
##molecule_type mRNA
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251-358 ##label EDI
                                                                                                      Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, DNA (1987) 6:461-472 Expression of human uterine tissue-type plasm in mouse cells using BPV vectors.
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Tissue plasminogen activator: peptide analyses confirm an indirectly derived amino acid sequnce, identify the act site serine residue, establish glycosylation sites, and
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Thromb. Haemost. (1988) 59:523-528
Isolation, identification and pharmacokinetic properties of human tissue-type plasminogen activator species: possible localisation of a clearance recognition site.
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Emtage, J.S.; Opdenakker, G.; Volckaert, G.; Rombauts
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NT Cleavage by plasmin or trypsin produces two chains held together b;
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##cross-references GDB:119496; OMIM:173370
#p_position 8p12-8p12
  ##residues 1-716 ##label
##cross-references GB:M74180;
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                                               ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 SYTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cleavage by plasmin or trypsin produces two chains held together by a single disulfide bond.

t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. It is active in tissue remodeling and destruction, particularly in fibrinolysis, and in cell migration.

t-PA binds chain A of fibrin by kringle 2 and the fibronectin type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of.
                                                                                                                                                                                                                                                                                   A40332 #type complete
macrophage-stmulating protein 1 precursor - mouse
hepatocyte growth factor-like protein
#formal_name Mus musculus #common_name house mouse
17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change
18-Jun-1999
                                                                            A40332
                                                                                                                                          Degen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry (1991) 30:9781-9791
Characterization of the mouse cDNA and gene coding
hepatocyte growth factor-like protein: expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.3%;
ilarity 37.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 510/3  
#superfamily tissue plasminogen activator; EGF homology; fibronectin type I repeat homology; kringle homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.; Schleuning, W.D.
J. Biol. Chem. (1985) 260:11223-11230
Isolation and characterization of the human tissue-type plasminogen activator structural gene including its 5' flanking region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I55232
Fisher, R.; Waller,
                                                                                                                                                                                                                                                                      A40332; B40332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fibrinolysis; glycoprotein; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotations omitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serine proteinase
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                                                                                                                         development
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#domain propeptide #status predicted #label PRO\
#product t-plasminogen activator #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 179; DB 1;
Pred. No. 1.12e-17;
15; Mismatches 23
DEG
NID:g193831;
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  PIDN:AAA50166.1;
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  PID:g193832
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ACCESSIONS
REFERENCE
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1-31
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Best Local Similarity
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489-709
72,173,305,620
                              #authors
#journal
#title
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110-186
191-268
292-370
379-457
                                                                                                                                                                                    #authors Schaller, J.; Moser, P.W.; Dannegger-Muller, Rosselet, S.J.; Kampfer, U.; Rickli, E.E. #journal Eur. J. Biochem. (198) 119:267-278 #title Complete amino acid sequence of bovine plasmi #cross-references MJID:85203906
                                                                                                                                                                      #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                                                                                                                                                                                                                                                                                                   cession ##molecule_type mRNA ##molecule_type mRNA ##residues 1-812 ##label BER ##cross-references EMBL:x79402; NID:g494962; PIDN:CAA55939.1; ##cross-references EMBL:x9494963
                                                                                                 ##molecule_type protein
##residues 27-334,'D',336-515,'H',517-554,'L',556-812
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1-18,'P',20-716 ##label DEG2
##cross-references GB:M74181; NID:g193833; PIDN:AAA50167.1; PID:g193834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264
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Malinowski, D.P.; Sadler, J.E.; Davie, E.W. Biochemistry (1984) 23:4243-4250 Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning and characterizatin $45046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berglund, L.; Andersen, M.D.; Petersen, T.E. submitted to the EMBL Data Library, May 1994 Cloning and characterizatin of the bovine plasminogen cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S45046
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30-Sep-1987 #sequence_revision 28-Apr-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasminogen
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plasmin (EC 3.4.21.7) precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predicted #length 716 #moi
                                                                                                                                                                        A25835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disulfide-bonded heterodimer of chains derived from the same
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#domain trypsin homology #label TRY\
#binding_site carbohydrate (Asn) (covalent) #status
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#domain kringle homology #label KR1\
#domain kringle homology #label KR2\
#domain kringle homology #label KR3\
#domain kringle homology #label KR3\
#domain kringle homology #label KR4\
#domain kringle homology #label KR4\
                                                                                                                                                                                                                                                                                                                                                   it is uncertain whether Met-1 or Met-8 is the initiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #product macrophage-stimulating protein 1 #status
experimental #label MAT\
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Pred. No. 6.75e-17;
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                                                                                                                         ##label SCH
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SUMMARY
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1-26
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CLASSIFICATION
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485-564

485-564

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584-805

56-80,60-68,

110-188 131-171,

119-188 131-171,

119-188 131-252,

195-323 213-252,

241-264 282-359,

303-342,331-344,

844-461 405-444,

844-461 405-444,

845-647,535-554,
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Best Local
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#title
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27-103
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#accession I45961
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104-583
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                                                                                351 WEYC 354
                                     107 WGYC 110
                                                                                                                                                                   294 VAVTESGHTCQRWSEQTPHKHNRTPENFPC-KNLEENYCRNPNGEKAPWC-YT-TNSEVR 350
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##rosidues 706-743,'R',745-812 ##label MAL
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                                                                                                                                                                                                                n 28.5%;
Similarity 35.9%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of processes including embryonic development, tissue remodeling and tumor invasion; in ovulation it weakens the walls of the graafian follicle; also activates the urokinase-type plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E Lergier, W.; Manneberg, M.; Gillessen, D. Eur. J. Biochem. (1981) 114:465-470 Comparison of the primary structure of the N-terminal fragments of human, bovine and porcine plasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *superfamily plasmin: kringle homology; plasminogen-related protein precursor homology; trypsin homology duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine proteinase; zymogen
                                                                                                                                                                                                                                                                                                          #length 812
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#binding_site carbohydrate (Ser) (covalent)
experimental\
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#domain kringle homology *label KR1\
#domain kringle homology *label KR2\
#domain kringle homology *label KR3\
#domain kringle homology *label KR3\
#domain kringle homology *label KR4\
#domain kringle homology *label KR5\
#domain plasmin chain B *status experimental *label BCH\
#domain trypsin homology *label TRY\
                                                                                                                                                                                                                                                                                                        #active_site His, Asp, Ser #status predicted
th 812 #molecular-weight 91215 #checksum 3
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#binding_site carbohydrate (Asn) (c
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#product plasminogen #status experimental #label PRO\
#domain activation peptide #status experimental #label
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                                                                                                                                                                                                                Score 174; DB 1; L
Pred. No. 1.06e-16;
11; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                         (Asn) (covalent) #status
                                                                                                                                                                                                                                                           Length 812;
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#accession Accession ###molecule_type mRNA 1-812 ##label DEG
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191-268
292-370
379-457
489-716
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72,305,620
                                                                                    #title Characterization of the cDNA coding localization of the gene to mouse #cross-references MUID:91184812
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#accession JC5061
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PID:e223604; PID:g1669719
disulfide-bonded heterodimer of chains derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                      107 WGYCD
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##residues 1-716 ##label OHS
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Local Similarity 33.8%;
les 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                 angiostatin; plasminogen
#formal_name Mus musculus #common_name house mouse
20.sep-1991 #sequence_revision 01-Nov-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; S. Hamaguchi, I.; Takasu, N.; Suda, T. Biochem. Biophys. Res. Commun. (1996) 227:273-280
                                                                                                                                                   Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, Genomics (1990) 8:49-61
                                                                                                                                                                                                                                                                                                                        PLMS #type complete plasmin (EC 3.4.21.7) precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #superfamily hepatocyte growth factor; kringle homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular cloning of rat macrophage-stimulating protein its involvement in the male reproductive system.
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macrophage-stimulating protein 1 precursor - rat
#formal_name Rattus norvegicus #common_name Norway rat
31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change
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predicted
#length 716 #molecular-weight 80733 #checksum
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#domain trypsin homology #label TRY\
#binding_site carbohydrate (Asn) (covalent) #status
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#domain kringle homology #label KRI1\
#domain kringle homology #label KRI2\
#domain kringle homology #label KRI3\
#domain kringle homology #label KRI4\
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#product macrophage-stimulating protein 1 #status
predicted #label MAT\
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Pred. No. 1.65e-16;
16; Mismatches 24
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                                                                                                           for mouse plasminogen and chromosome 17.
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377-454,398-437,
426-449,481-560,
502-543,531-555,
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152-176,185-262,
188-316,206-245,
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##residues 20-25 ##label LIJ
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##residues 22-27 ##label LI2
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Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostatin. Together with endostatin (see PIR:A56101, angiostatin acts to inhibit angiogenesis, and so may be useful in treating solid tumors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of processes including embryonic development, tissue remodeling and tumor invasion; in ovulation it weakens the walls of the graafian follicle;
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Characterization of the murine plasma fibrinolytic system.
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#domain kringle homology #label KR1\
#domain kringle homology #label KR2\
#domain kringle homology #label KR3\
#domain kringle homology #label KR4\
#domain kringle homology #label KR4\
#domain kringle homology #label KR5\
#domain kringle homology #label KR5\
#domain chain B #status predicted #label BCH\
                              #cleavage_site Thr-Val
predicted\
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#domain activation peptide #status predicted #label APT\
#product angiostatin #status predicted #label AST\
#product plasmin #status predicted #label MAT\
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(plasminogen activator) #status
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KEYWORDS
FEATURE
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Matches
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#title Primary structure of guinea-pig Hageman fact
around the cleavage site differs from the
#cross-references MUID:93003367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.2%;
Best Local Similarity 36.9%;
Matches 24; Conservative
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216-294
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 VSVTVSGKTCQRWSEQTPHRHNRTPENFPC-KNLEENYCRNPDGETAPWCYTTDSQLR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 WEYCE 348
                                                                                                                                                                                                                                                                                                                                              5
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 VSVTDFGAPCLRWAEVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                              GAPCLRWAEVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVDWGYCD 111
                                                                                                                                                                                                                                                                                                                                                                                                                       h 28.0%;
Similarity 37.3%;
22; Conservative
Fibrinolysis (1987) 1:91-102
Amino acid sequence of the heavy chain of porcine plasmin.
Comparison of the carbohydrate attachment sites with the
                                                            Schaller, J.; Marti, T.; Rickli, E.E.
                                                                                                                      S03733; S03737; A25834
                                                                                                                                         07-Sep-1990 #sequence_revision 18-Jul-1997
                                                                                                                                                                                                                        plasminogen
                                                                                                                                                                                                                                         plasmin (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hageman factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $28941 #type fragment
coagulation factor XIIa ()
                                                                                                                                                         #formal_name Sus scrofa domestica #common_name domestic
07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Cavia porcellus #common_name guinea pig
25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #length 812 #molecular-weight 90846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #length 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain fibronectin type II repeat homology #label IF2\
#domain fibronectin type I repeat homology #label FB1\
#domain kringle homology #label KRC\
#domain trypsin homology #label TRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #active_site His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          experimental\
                                                                                                                                                                                                                                         #type fragment: 3.4.21.7) pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #checksum 8522
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 171; DB 2;
Pred. No. 4.04e-16;
12; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 2.58e-16;
11; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XIIa (EC 3.4.21.38) - guinea pig
                                                                                                                                                                                                                                           precursor -
                                                                               Roesselet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                           pig (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 603;
                                                                          S.J.; Kaempfer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibuya, Y.; Tanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor: sequence
the human molecule
                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω
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                                                                                                                                                                              pig
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FEATURE
1-790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #pathway
CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                   Best Local
Matches
                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                       187-226,215-238,
256-333,277-316,
305-328,358-435,
379-418,407-430,
461-540,482-523,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461-540
561-790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78-560
84-162
166-243
256-333
358-435
450-790
                                                                                                                                                                                                                                        511-535,547-665,
557-565,587-603,
679-746,709-725,
                                                                                                                                                                                                 602,645,740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #title Comparison of the primary structure of the N-terminal CNBr fragments of human, bovine and porcine plasminogen.
#cross-references_MUID:81212097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                              54,34-42,84-16
-145,133-157,
6-243,169-297,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cession ALJUU.##molecule_type protein 450-790 ##label MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oss-references MUID:85203907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type protein
##residues 1-57 ##label BRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues
                                        268 VSVTASGHTCQRWSAQSPHKHNRTPENFPC-KNLEENYCRNPDGETAPWC-YTTD-SEVR 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type protein
    47
                                                                                                                                                                                                                                                                                                                                                                                                                                                              34-42,84-162,
VSVTDFGAPCLRWAEVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVD 106
                                                                                   h 28.0%;
Similarity 37.5%;
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of processes including embryonic development, tissue remodeling and tumor invasion; in ovulation it weakens the walls of the graafian follicle; also activates the urokinase-type plasminogen activator
                                                                                                                                                                      #disulfide_bonds #status
#active_site His, Asp, Se
#length 790 #checksum 3770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #superfamily plasmin; kringle homology; plasminogen-related
protein precursor homology; trypsin homology
fibrinolysis; glycoprotein; hydrolase; kidney; kringle;
plasma; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. (1985) 149:279-285
Determination of the complete amino-acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A25834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunisholz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S03735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrinolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               miniplasminogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.;
Lergier, W.; Manneberg, M.; Gillessen, D.
ur. J. Biochem. (1981) 114:465-470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and bovine species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain trypsin homology #label TRY\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #product plasmin chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain kringle homology #label KR5\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #product miniplasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain activation peptide #status predicted #label APT\
#product plasmin chain A #status predicted #label ACH\
#domain kringle homology #label KR1\
#domain kringle homology #label KR2\
#domain kringle homology #label KR3\
#domain kringle homology #label KR3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #domain plasminogen-related
  (fragment) #label PLPH\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product plasminogen #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-560 ##label SCH
                                                                                   Score 171; DB 1; Le Pred. No. 4.04e-16; B; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                             Ser #status predicted
                                                                                                                                                                                                               predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #status experimental #label
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protein precursor homology
                                                                                                                              Length 790
                                                                                     Indels
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ACCESSIONS
REFERENCE
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ENTRY
TITLE
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                                                          CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARY
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                                ORGANISM
                                                                                 ALTERNATE_NAMES
                                                                                                                                   ENTRY
                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##ccession A61329
##molecule_type protein
##molecule_type protein
10-16,'X',18-19;525-550 ##label FUJ
##residues
10-16,'X',18-19;525-550 ##label FUJ
##residues
10-16,'X',18-19;525-550 ##label FUJ
##residues
10-16,'X',18-19;525-550 ##label FUJ
##residues
ASSIFICATION #superfamily coagulation factor XII; EGF homology;
fibronectin type II
repeat homology; Kringle homology; trypsin homology
repeat homology; Kringle homology; trypsin homology
blood coagulation; fibrinolysis; glycoprotein; hydrolase;
prudORDS
blood coagulation; fibrinolysis; glycoprotein; hydrolase;
prudORDS
blood coagulation; fibrinolysis; glycoprotein; hydrolase;
                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125-160
207-287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #authors
#journal
#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:94242782
#accession $45281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350-587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 WDYC
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                                                                                                                                                                                                                                 53
                                                                                                                                                                                                                                                                                                                                                     y Match 27.7%;
Local Similarity 38.3%;
                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                            110
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JC4795 #type complete
plasma hyaluronan-binding protein precursor - human
hepatocyte growth factor activator-like protein; PHBP
serine proteinase (EC 3.4.21.-)
#formal_name Homo sapiens #common_name man
15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hageman factor (activated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujikawa, K.; Walsh, K.A.; Davie, Biochemistry (1977) 16:2270-2278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shibuya, Y.; Semba, U.; Okabe, H.; Kambara, T.; Yamamoto, T. Biochim. Biophys. Acta (1994) 1206:63-70 Primary Structure of bovine Hageman factor (blood coagulation factor XII): comparison with human and guinea pig
                                                                                                                                                                                                                                                                                                                                                                                                                            #length 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolation and characterization of bovine factor XII (Hageman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $45281; A61329
$45281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #formal_name Bos primigenius taurus #common_name cattle
10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S45281 #type fragment coagulation factor XIIa (EC 3.4.21.38) precursor - bovine
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                              #domain fibronectin type II repeat homology
#domain fibronectin type I repeat homology #
#domain kringle homology #label KRG\
#domain trypsin homology #label TRY\
#active_site Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the authors translated the codon GAG for residue 23 as Val, GAG for residue 70 as Asp, AAG for residue 171 as Met, CTT for residue 143 as His, GAC for residue 177 as Gly, GCC for residue 191 as Pro, CTC for residue 203 as Phe, GTG for residue 247 as Leu, CCG for residue 286 as Gln, AAC for residue 348 as Ile, GAC for residue 370 as Val, CAA for residue 371 as His, CAG for residue 415 as His, and ATC for residue 505 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-593 ##label SHI
                                                                                                                                                                                                                                                                                                                                                                                                                                 #checksum 1172
                                                                                                                                                                                                                                                                                                                            Score 169; DB 2;
Pred. No. 9.83e-16;
12; Mismatches 19
                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E.W.
                                                                                                                                                                                                                                                                                                                                                                          Length 593;
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#label FB1\
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                                                                                                           DATE
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115-125,120-136,
138-147,154-165,
159-176,178-187,
04-276,215-257,
6-271,301-435,
7-363,355-424,
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115-147
154-187
                      #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [47-515,477-493,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references GDB:4573962

a disulfide-bonded heterodimer of chains produced same precursor; the catalytic chain is degraded chain lacking the active site serine residue superfamily plasma hyaluronan-binding protein; EG kringle homology; trypsin homology chondroitin sulfate proteoglycan; glycoprotein; gr factor; hyaluronic acid; hydrolase; kringle; pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##experimental_source plasma
##note parts of this sequence, including the amino ends of the
#mote mature chains, were determined by protein sequencing
                                                                                                                                                                                                                                                                                                 243 HNFCRNPDADEKPWCFIKVTNDKVKWEYCD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-560 ##label CHO
##cross-references GB:S83182; NID:g1836158; PIDN:AAB46909.1;
PID:g1836159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
                                                                                                                                                                                                                                                         82 HNFCRSPDGAGRPWCFYGDARGKVDWGYCD 111
                                                                                                                                                                                             14
Hashimoto,
Nakano, N
                                                                                JC5878 #type complete
plasma hyaluronan-binding protein precursor - mouse
#formal_name Mus musculus #common_name house mouse
11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                #length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDB: HABP2; HABP; PHBP; HGFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Purification and characterization of a novel hyaluronan binding protein (PHBP) from human plasma: It has three EGF, a kringle and a serine protease domain, similar to hepatocyte growth factor activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mazda, T.; Tomita, M.
J. Biochem. (1996) 119:1157-1165
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                                                                                                                                                                                                                                                                                                                                              Conservative
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#active_site His, Asp, Ser #status predicted
#th 560 #molecular-weight 62671 #checksum 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #domain signal sequence #status predicted #label SIG\
#product plasma hyaluronan-binding protein, 50K chain
#status predicted #label 50K\
#domain EGF homology #label EGI\
#domain EGF homology #label EGS\
#domain EGF homology #label EGS\
#domain Kringle homology #label KRI\
#domain kringle homology #label TRY\
#domain trypsin homology #label TRY\
#domain trypsin homology #label TRY\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #product plasma hyaluronan-binding protein, catalytic
chain #status predicted #label CAT\
#binding_site carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                              27.3%; 56.7%;
Y.; Choi-Miura,
                                                                                                                                                                                                                                                                                                                                                                Score 167; DB 1;
Pred. No. 2.39e-15
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                                                                                                                                                                                                                                                                                                                                              Mismatches
Sumiya,
Tomita,
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                                                                                                                                                                                                                                                                                                                                                                                  Length 560
                 Saguchi,
                 Κ.;
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plasma; serine
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to a
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FEATURE
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#authors
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1-23
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                      18-29
30-559
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113-145
152-185
152-274
312-558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal
#title
                                                                                                                                                                                                                                                        #authors Ny, T.; Leonardsson, G.; Hsue plasminogen activator. #cross-references MUID:89170114 #accession A31597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #cross-references MUID:90130448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal Biol. Pharm. Bull. (1997) 20:1127-1130
#title Cloning of the cDNA for a mouse homologue
novel hyaluronan-binding protein.
#cross-references_MUID:98065239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312-548
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                                                                                                                                               ##residues 1-379,/K',381-559 ##label NYT 1-379,/K',381-559 ##label NYT ##cross-references GB:M23697; NID:g530159; PIDN:AAA41812.1; PID:g530160 ##superfamily tissue plasmingen activator; EGF homology; fibronectin type I repeat homology; kringle homology;
                                                                                                                                                                                                                                   ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-559 ##label
##cross-references GB:M31197;
GB:J05226
                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
##residnee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 HNFCRNPDGDHKPWCFVKVNSEKVKWEYCD 270
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Similarity 60.0%;
18; Conservative
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#superfamily plasma hyaluronan-binding protein;
kringle homology; trypsin homology
                                                                                                                    trypsin homology fibrinolysis; glyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A35029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feng, P.; Ohlsson, M.; NY, T.
J. Biol. Chem. (1990) 265:2022-2027
The structure of the TATA-less rat tissue-type plasminogen activator gene. Species-specific sequence divergences in the promoter predict differences in regulation of gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A35029 #type complete
t-plasminogen activator (EC 3.4.21.68) precursor - rat
#formal_name Rattus norvegicus #common_name Norway rat
10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                             A31597
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                                                                                                  proteinase
#domain signal sequence #status predicted #label SIG\
#domain propeptide #status predicted #label PRO\
#product t_plasminogen activator #status predicted
#label MAT\
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#product plasma hyaluronan-binding protein large chain
#status predicted #label MATI\
#domain EGF homology #label EG1\
#domain EGF homology #label EG2\
#domain EGF homology #label EG3\
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#product plasma hyaluronan-binding protein small chain
#status predicted #label MATS\
                                                                                                                  glycoprotein; hydrolase;
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Pred. No. 5.78e-15;
2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                 FEN NID:9207429; PIDN:AAA42261.1; PID:9207431;
                                                                                                                                                                                                                                                                                                                                                        G.; Hsueh, A.J.W.
                                                                                                                                                                                                                                                                                                                   of a cDNA for
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                                                                                                                  kringle; serine
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SUMMARY
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Best Local Similarity 41.0%;
Matches 25; Conservative
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83-116
124-205
213-294
209-539
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88-105,107-116,
124-205,145-187,
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                                                                                                                                              8-309
                                                                        111 D 111
                                                                                                             290 D 290
                                                                                                                                                                                                                                                                                               #cleavage_site Arg-Ile (plasmin, trypsin) #status
predicted\
#active_site His, Asp, Ser #status predicted
#length 559 #molecular-weight 62903 #checksum 8573
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#binding_site carbohydrate (Asn) (covalent) #status
predicted\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain trypsin homology #label TRY\
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#domain EGF homology #label EGF\
#domain kringle homology #label KR1\
#domain kringle homology #label KR2\
#product t-plasminogen activator chain B #status
predicted #label BCH\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #product t-plasminogen activator chain A #status
predicted #label ACH\
                                                                                                                                                                                                                         Score 164; DB.1; Length 559;
Pred. No. 8.98e-15;
12; Mismatches 19; Indels
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US-09-147-947-6-02.15p USCINTS 293

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

₫ď protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:21:05 2000; MasPar time 5.46 Seconds 399.446 Million cell updates/sec

Description: Perfect Score:

Title: >US-09-147-947-6 (40-112) from US09147947A.pep (2 of 6) 611

Sequence: 1 CPAGEPWVSVTDFGAPCLRW.....RPWCFYGDARGKVDWGYCDC 73

Scoring table: PAM 150 Gap 11

Searched:

82229 segs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38

Statistics: Mean 37.173; Variance 60.386; scale 0.616

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19 156 25.5 169 20 154 25.2 1420 21 150 24.5 655 22 149 24.4 810	156 25.5 154 25.2 150 24.5	156 25.5 154 25.2	156 25.5	10.	157 25 7	161 26.4	161 26.4	161 26.4	161 26.4	163 26.7	164 26.8	169 27.7	28.0	171 28.0	172 28.2	174 28.5	175 28.6	179 29.3	179 29.3	185 30.3	507 83.0	100.0	Score Match Length
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	N PRECUE		ے	PLASMINOGEN (EC 3.4.21	APOLIPOPROTEIN(A) PREC	PLASMINOGEN PRECURSOR		GROWTH	GROWTH	HEPATOCYTE GROWTH FACT	TISSUE PLASMINOGEN ACT	COAGULATION FACTOR XII	PLASMINOGEN (EC 3.4.21		PLASMINOGEN PRECURSOR	PLASMINOGEN PRECURSOR	HEPATOCYTE GROWTH FACT	TISSUE PLASMINOGEN ACT	TISSUE PLASMINOGEN ACT	COAGULATION FACTOR XII	NEUROTRYPSIN PRECURSOR	NEUROTRYPSIN PRECURSOR	Description
1	786-	e-1	.67e-1	.43e-	3.99e-15	.86e-1	.86e-1	.86e-1	.86e-1	.23e-1	₽	.21e-1	4.57e-18	.57e-1	.80e-1	.05e-1	2e-1	.93e-2	.93e-	.54e	1.24e-97	1.14e-123	Pred. No.

45	44	43	42	41	40	39	3 8	37	36	35	34	ω G	32	31	30	29	28	27	26	25	24	
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2.12e-02	9.86e-03	6.71e-03	1.27e-06	1.27e-06		6.14e-08	6.14e-08	1.05e-08	1.05e-08	6.75e-09	4.32e-09	1.77e-09	7.18e-10	4.57e-19	.84e-	2.96e-11	.96e-	.87e-	1.18e-11	4.68e-12	1.16e-12	

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EMBL: AJ001531; CAA04816.1;	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinfor the European Bioinformatics Institute, use by non-profit institutions as lon modified and this statement is not remove entities requires a license agreement (Sor send an email to license@isp-sib.ch).	LEARNING AND MEMORY - SUBCELLULAR LOCATION - SIMILARITY: BELONGS - TRYPSIN FAMILY SIMILARITY: CONTAINS - SIMILARITY: CONTAINS	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=BRAIN; MEDLINE; 98201705. MEDLINE; 98201705. PROBA K., GSCHWEND PCLONING and seque Biochim. Biophysi- FUNCTION: PLAY ACTION MAY CITAY	ETR_HUMA 5-6730; 5-DEC-19 5-DEC-19 5-DEC-19 EUROTRYP RSS12. omo sapi utheria;
001531; CP PS00134; PS00135; PS00420; e; Serine 21 23 387	S-PROT entr the Swiss I the Swiss I ean Bioinfo non-profit and this st and this st an email to	G AND NULAR LO	FROM N.A. RAIN; 98201705. GSCHWEND and sequen Biophys. PLAY	(Re (Re (Re (Re (Re (Re
CAA04816.1; ; TRYPSIN_HIS; 1. ; TRYPSIN_SER; 1. ; SEPRACT_RECEPPOR; 3. ; SEPRACT_RECEPPOR; 3. ; SEPRACT_RECEPPOR; 3. POTOTENTIAL 875 POTOTENTIAL NUBUROTRYP PROLINE-R 165 KRINGLE. 271 SRCR 1. 381 SRCR 2. 487 SRCR 3.	s SWISS-PROT entry is copyright. It is produce the Swiss Institute of Bioinformatics European Bioinformatics Institute. There by non-profit institutions as long as lified and this statement is not removed. Unlities requires a license agreement (See htt.) send an email to license@isp-sib.ch).	HO SPE	T.P., ncing c Acta 13 S A ROI	→ fotototo H
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in; SIN.	e e d	(BY SIMILARITY) . SE FAMILY S1; AL: DOMAIN.	P.; encoding 1998). ECBCANTS	875 AA. update) on update) (MOTOPS) (MOTOPS ata; Vert
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GSCHWEND T.P., KRUEGER
"Neurotrypsin, a novel
nervous system.";
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15-DEC-1999 (Rel. 39, Last
NEUROTRYPSIN PRECURSOR (EC
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DOMAIN
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aryota; Metazoa; C
heria; Rodentia; S
                                                                                                                                                                                  SIMILARITY: CONTAINS 1 KRINGLE DOMAIN. SIMILARITY: CONTAINS 3 SRCR DOMAINS.
                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: SECRETED. SIMILARITY: BELONGS TO PEPTIDASE
                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL
                                                                                                                                                                                                                                                                                                                               CHEM. Biophys. Res. Commun. 239:386-392(1997).
FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH LEARNING AND MEMORY OPERATIONS.
                                                                                                                                                                                                                            TRYPSIN FAMILY
                                                                                                                                                                                                                                                                                                AND AMYGDALA.
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Y., YAMAS
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Last annotation update)
R (EC 3.4.21.-) (MOTOPSIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K., TSURUOKA N., NAKAZATO H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
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SERINE PROTEASE.
ZYMOGEN ACTIVATION REGION.
REACTIVE BOND (POTENTIAL).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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67D5272B CRC32;
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lae; Murinae;
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Mus.
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EMBL; D89871; BAA23986.1; -
MGD; MGI:1100881; PRSS12.
PFAM; PF00530; SRCR; 3.
PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FA12_HUMAN STAN
P00748;
P00748 (Rel. 0
01-OCT-1989 (Rel. 1
01-NOV-1997 (Rel. 3
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               SEQUENCE OF 14-615 FROM MEDLINE; 86033830.
COOL D.E., EDGELL C.J.S. MCGILLIVRAY R.T.A.;
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"Characterization of the hyman blood coagulation intron/exon gene organization and analysis of the region.";
                                                                                                               Nucleic Acids
                                                                                                                                                   TRIPODI M., CITARELLA F., CORTESE R.;
                                                                                                                                                                                        SEQUENCE OF 4-615 FROM N. MEDLINE; 86176794.
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COAGULATION
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PROSITE; PS00134; TRYPSIN, HIS; 1.
PROSITE; PS00135; TRYPSIN, SER; 1.
PROSITE; PS00420; SPERACT_RECEPTOR; 3.
                                                                                                                                                                                                                                                                                                                                             MEDLINE;
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 'Characterization
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                                                                                                             sequence coding for human coagulation ic Acids Res. 14:3146-3146(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity ;
57; Conserve
                                                                                                                                                                                                                                             Chem. 262:13662-13673(1987)
                                                                                                                                                                                                                                                                                                                                             88007593
               EDGELL C.J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease; Glycoprotein; Kringle; Repeat;
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12, Last sequence update)
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R XII PRECURSOR (EC 3.4.21.38)
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78.1%;
   human blood
                                                                          N.A.
                                                                                                                                                                      GUIDA
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                                       LOUIE
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REACTIVE BOND (POTENTIAL).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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Pred. No. 1.24e-97;
9; Mismatches 7;
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                                   G.V.,
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S
coagulation
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                                   ZOLLER M.J.,
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                                                                                                                                                                                                                                                                                  factor XII gene
e 5'-flanking
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                                       BRAYER
                                                                                                                                 XII (Hageman).";
                                     G.D.,
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RT RALES RAL

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REPLINE, 92184750.

RA HARRIS R.J., LING V.T., SPELLMAN M.W.;

RA HARRIS R.J., LING V.T., SPELLMAN M.G.L.,

RATION OF BRADYKININ NAD ANGIOTENSIN THAT PARTICIPATES IN F12 DO NOT CAUSE ANY CLINICAL SYMPTOMS. THE SELECTIVELY AND HAW KININGEN FORM A COMPLEX BOUND TO AN ANIONIC SURFACE. PREKALLIKREIN IS CLEAVED BY FACTOR XII TO FORM KALLIKREIN, WHICH THEN CLEAVED BY FACTOR XII AND THEN THEN CLEAVED BY FACTOR XII AND THEN THEN CLEAVES FACTOR XII FIRST CONTAINS 1 FIRSTORN TYPE-I DOMAIN.

CC. -I. SIMILARITY: CONTAINS 1 FIRSONECTIN TYPE-I DOMAIN.

CC. -I. SIMILARITY: CONTAINS 1 KRINGLE REGION.

CC. -I. SIMILARITY: CONTAINS 1 KRINGLE REGION.

CC. -I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE FAMILY S1; ALSO KNOWN AS THE CONTAINS 1 KRINGLE
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MEDLINE; 83291041.
FUJIKAWA K., MCMULLEN B.A.;
"Amino acid sequence of human beta-factor XIIa.";
"Amino acid sequence of 1933(1983).
                                                      between
the Euro
                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 90046788.
MIYATA T., KAWABATA S.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT WASHINGTON MEDLINE; 90046788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Amino acid sequence of the heavy chain (activated Hageman factor).";
". Biol. Chem. 260:5328-5341(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 20-379
MEDLINE: 85182674.
MCMULLEN B.A., FUJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 86216049.
QUE B.G., DAVIE E.W.;
"Characterization of factor).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prediction of the primary structure of factor XII and the tertiary structure of beta-factor XIIa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOVINGA J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Coagulation factor XII
factor XIIa results fro
Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAITO H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT LOCARNO. MEDLINE; 94325559
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                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its European Bioinformatics Institute as a long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid substitution Arg-353-->Pro leading
likrein cleavage site.";
od 84:1173-1181(1994).
                                                                                                                    TRYPSIN FAMILY.
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and this statement is not ren
requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHALLER J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUJIKAWA
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from Cys-571-->Ser substitution.";
ci. U.S.A. 86:8319-8322(1989).
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                         not removed.
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         moved. Usage by and for commercial (See http://www.isb-sib.ch/announce)
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PROSITE; PS00135; FIBRONE
PROSITE; PS01253; FIBRONE
PROSITE; PS01253; FIBRONE
PROSITE; PS0070; KRINGLE
PRAM; PF00008; EGG; 2.
PRAM; PF00040; fn2; 1.
PFAM; PF00040; fn2; 1.
PFAM; PF00040; fn2; 1.
PFAM; PF00040; trypsin; 1.
PFAM; PF00051; kringle; 1.
PFAM; PF00051; kringle; 1.
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EMBL; M11723; AAA51986.1;
EMBL; M17466; AAB59490.1;
EMBL; M17464; AAB59490.1;
EMBL; M17465; AAB59490.1;
EMBL; M13147; AAA70224.1;
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                                        VARIANT
                                                                                     DISULFIL
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TRYPSIN_HIS; 1
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EGF_1; 2.
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KRINGLE_2; 1.
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ysis; S¶gnal;
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R -> P (IN LC. 3)
/FTIG=VAR_006623
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BETA-FACTOR XIIA PART
FIBRONECTIN TYPE-II.
EGF-LIKE 1.
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                                                                     INACTIVE).
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(BY)
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Repeat; Zymogen;
                                        DC; INACTIVE)
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SIMILARITY).
SIMILARITY).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UROT_MOUSE
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through etween the Swiss Institute of Bioinformatics and the Event of British and the Event of British are no restricted by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RICKLES R.J., DARROW A.L., STRICKLAND S.;
"Molecular cloning of complementary DNA to
activator mRNA and its expression during FS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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1-JUL-1989 (Rel. 11, Last sequence update)
1-JUL-1989 (Rel. 35, Last annotation update)
TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: TPA CONVERTS PLASMINGEN TO PLASMIN BY HYDROLYZING A SINGLE R-V BOND IN PLASMINGGEN. ACTIVE IN TISSUE REMODELING AND DESTRUCTION, PARTICULARLY IN FIBRINOLYSIS, AND IN CELL MIGRATION CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN PLASMINGGEN TO FORM PLASMIN.

MISCELLANEOUS: TPA ATTACHES TO THE KRINGLE STRUCTURE OF THE A
                                                                                                                                                                                                                                                                                                                                        CHAIN OF FIBRIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-I DOMAIN.

SIMILARITY: CONTAINS 2 KRINGLE REGIONS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO
                                                                                                                                                                                                                                                                                                                               TRYPSIN FAMILY.
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                           PF00008; EGF; 1.
PF00039; fn1; 1.
PF00051; kringle;
   PF00089; trypsin; 1.
inogen activation; Hydrolase;
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26; Conse
                                                                   PS01253; FIBRONECTIN_1;
PS00021; KRINGLE_1; 2.
PS50070; KRINGLE_2; 2.
                                                                                                         PS00134; TRYPSIN_HIS;
PS00135; TRYPSIN_SER;
PS00022; EGF_1; 1.
PS01186; EGF_2; 1.
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llarity 42.6%;
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Sciurognathi; Muridae;
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No. 4.54e-21
   Serine protease; Glycoprotein;
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ae; Murinae;
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P0075; Q15103;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68)
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  SEQUENCE FROM N.A. TISSUE=FETAL LUNG;
                                                                      GOEDDEL D.V., COLLEN D.;
"Cloning and expression o
cDNA in E. coli.";
Nature 301:214-221(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
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DOMAIN
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                                                                                                                                                                                                                                                   TISSUE=MELANOMA;
                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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                                                                                                                                                                       KOHR W.J.,
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FIBRONECTIN TYPE-I.
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                                                                                                                    tissue-type plasminogen activator
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SEEBURG P.I
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MEDLINE;
POHL G.,
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gecreted by human embryonic lung diploid fibroblasts, IMR-90
Agric. Biol. Chem. 55:1225-1232(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [7].
PFEIFFER G. SCHMIDT M., STRUBE K.-H., "Carbohydrate structure of recombinant plasminogen activator expressed in mous Eur. J. Biochem. 186:273-286(1989).
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MEDLINE, 86196143.
DEGEN S.J.F., RAJPUT B., REICH E.;
The human tissue plasminogen activator
J. Biol. Chem. 261:6972-6985(1986).
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SIEBERT P.D., FONG K.;
                                                                                                                                                                                               establish glycosylation sites, as Biochemistry 23:3701-3707(1984).
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Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 86284200.
HARRIS T.J., PATEL T.,
OPDENAKKER G., VOLCKAEJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression of human mouse cells using BPV DNA 6:461-472(1987).
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"Nucleotide sequence of the tissue-typ
from human fetal lung cells.";
Nucleic Acids Res. 16:5695-5695(1988).
                                      MEDLINE; 90092112
PFEIFFER G., SCHM
                                                                                                                                                        SEQUENCE FROM N.A. (SMALL TISSUE-UMBILICAL VEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HARRIS T.J., PATEL T., MARSTON F.A., LITTLE S., EMTAGE OPDENAKKER G., VOLCKAERT G., ROMBAUTS W., BILLIAU A., S "Cloning of cDNA coding for human tissue-type plasminog and its expression in Escherichia coli.";
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                                                                   STRUCTURE
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                                                                                                      "Variant tissue-type plasminogen activator (PLAT) cDNA obtained human endothelial cells.";
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                                       SCHMIDT M.,
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"Kringle-2 domain of the tissue-type assignments and secondary structure." Eur. J. Biochem. 197:155-165(1991).
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VLAHOS C.J., WILHELM O.G., HASSELL T., JASKUNAS S.R., B Plasminogen activator produced in Escherichia coli."; J. Biol. Chem. 266:10070-10072(1991).
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SMITH B.O., DOWNING A.K., DRISCOLL P.C., DUDGEON T.J., CAMPBELL I.

"The solution structure and backbone dynamics of the fibronectin to the solution structure and backbone dynamics of the fibronectin to the solution structure and backbone dynamics of the fibronectin to the solution of the solution
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Structure 3:823-833(1995)
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"Solution structure of the
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SUBUNIT: CLEAVAGE AFTER ARG-310 BY PLASMIN OR TRYPSIN RESULTS IN A TWO-CHAIN FORM OF THE MOLECULE. THESE TWO HALVES ARE HELD TOGETHER BY ONE OR MORE DISULFIDE MODDS.

ALTERNATIVE PRODUCTS: *HERE EXISTS A SHORT VARIANT PROBABLY DUE ALTERNATIVE SPLICING OF THE SAME GENE.

MISCELLANEOUS: TPA ATTACHES TO THE KRINGLE STRUCTURE OF THE A
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EMBL; M18182; I
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EMBL; L00153; I
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-i- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTICHERACTERISTIC OF SERINE PROTEASES CATALYT
                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BALB/C; TIS MEDLINE; 92002017.
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Eukaryota; Metazoa;
Eutheria; Rodentia;
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1-AUG-1992 (Rel. 23, Last sequence update)
5-JUL-1998 (Rel. 36, Last annotation update)
HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR
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                                          CONSERVED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRINGLESIS.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-I DOMAIN.

SIMILARITY: CONTAINS 2 KRINGLE REGIONS.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO
DEVELOPMENTAL STAGE: IS EXPR
JUST BEFORE BIRTH THE LEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN OF FIBRIN.

PHARMACEUTICAL: AVAILABLE UNDER THE NAMES ACTIVASE (GENENTECH)

AND RETAVASE (CENTOCOR AND ROCHE) [RETAVASE IS A FRAGMENT OF TO

THAT CONTAINS KRINGLE 2 AND THE PROTEASE DOMAIN; IT WAS ALSO KE

AS BM 06.022]. USED IN ACUTE MYOCARDIAL INFARCTION (AMI), IN ACUTE MYOCARDIAL INFARCTION (AMI), IN ACUTE MYOCARDIAL TOTAL TO INITIATES

ISCHEMIC STROKE (AIS) AND PULMONARY EMBOLISM (PE) TO INITIATES
                               ADRENAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WWW-"http://www.centocor.com/retavase.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WWW="http://www.genentech.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DWGYCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLTESGASCLPWNSMILIGKVYTAQNPSAQALGIGKHNYCRNPDGDAKPWCHVLKNR-RL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVTDFGAPCLRWAEVPPFLER-SPPASWAQLRGQ-RHNFCRSPDGAGRPWCFYGDARGKV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L00141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
25; Conser
                                                                                                                                                                                                            us (Mouse).
Metazoa; Chordata; Cranz
Metazoa; Sciurognathi; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of,
                                             SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.3%;
larity 37.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA36800.1; -.; AAA98809.1; -.; AAB59510.1; -.; AAB59510.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA30302.1;
AAA36800.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME-Retavase; NOTE-Clinical information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME-Activase;
                                                                                                                                                                                  TISSUE-LIVER
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                             LIVER.
 IS EXPRESSED AT LOW LEVELS DURING LEVEL INCREASES DRAMATICALLY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               omitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 179; DB:
Pred. No. 8.93e:
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE-Clinical information on Ach.com/Medicines/activase_insert.
                                                                        PROTEOLYTIC ACTIVITY, SINCE CRUCIAL PROTEASES CATALYTIC SITES ARE NOT
                                                                                                                                                                                                                                             Craniata;
                                             LOWER
                                                                                                                                                                                                                                Muridae;
                                             LEVELS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY S1; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                   716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
).93e-20;
                                                                                                                                                                                                                               Vertebrata;
ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                   MISON C.S.;
coding for a
g development.
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                                            LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 562;
                                                                                                                                                                                                                                                                                                         (MACROPHAGE
                                                                                                                                                                                                                               Mammalia;
                                             PLACENTA
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 RING GESTATION
AND REMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on Activase;
nsert.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on Retavase;
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                                                                                                                      hepatocyte .";
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VSVTDFGAPCLRWAEVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVD 106

260

REFCD

264

WGYCD

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Best Local
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EMBL; M74181;
HSSP; P00747;
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CONFLICT
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STABLE AFTERWARDS.
-!- PTM: MAY BE CLEAVED
HELD TOGETHER BY DIS
                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00051; PFAM; PF00089;
                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                 Kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00021; KRINGLE_1; PROSITE; PS50070; KRINGLE_2;
 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS SIMILARITY: BELONGS TRYPSIN FAMILY. BELON
VDVTESGRECQRWDLQHPHSHPFQPEKFLD-KDLKDNYCRNPDGSERPWCYTTDP--NVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:96080; HGFL.
                    Similarity
23; Conse
                                                            716
                   28.6%;
larity 35.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 PMK.
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AAA50167.1;
                                                                                                                                                                                                                                                                                                                                                                                                                         trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                    kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VED AFTER AA 488,
DISULFIDE BONDS,
                                                                                                                                                                                                                                                                                                                                                                                                                Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S 4 KRINGLE REGIONS.
TO PEPTIDASE FAMILY S1:
ONGS TO THE PLASMINOGEN
                                                            ₩;
                 Score 175; DB 1; Len
Pred. No. 6.42e-19;
Pred. "-+ches 26;
                                                                                                                                                                                                                                                                  KRINGLE 1.

KRINGLE 2.

KRINGLE 3.

KRINGLE 4.

SERINE PROTEASE-LIKE.

SERINE PROTEASE-LIKE.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                       INTERCHAIN (BY )
BY SIMILARITY
                                                           POTENTIAL.
P -> Q (IN
EDDAD87F
                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4
                                                                                                                                                                                                                                                                                                                                                                                           HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                      protease homolog; Signal
POTENTIAL.
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                                                            GENOMIC CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as its content
                                                                                                                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBFAMILY
                                      Length
                                                                      SEQUENCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALSO
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                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in no way
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FTT DRR KW
                                                                                                                                                                                                                                                                                                                                                                                                                                      Thuman and bowline plasminogen.";

12 Blochemistry 23:4243-4250(1984).

23 -1 FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS PROTECURIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLIDING EMBRYONIC DEVELOPMENT, TISSUE REMOBELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND CS. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, CLAMININ AND VON WILLEBRAND FACTOR.

24 C -!- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CRANNOT BE ACTIVATED WITH STREDTOKINASE.

25 -!- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IS INMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

26 -!- SIMILARITY: BELONGS TO THE PLASMINOGEN SUBFAMILY.

27 - SIMILARITY: BELONGS TO THE PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                    EMBL; X79402; CAA55
EMBL; K02935; AAA30
PIR; A25835; PLBO.
HSSP; P00747; 2PK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P06868; 028162;
01-JAN-1988 (Rel. 06, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PLASMINOGEN PRECURSOR (EC 3.4.21.7).
                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SCHALLER J., MOSER P.W., DANNEGGER-MULLER G.A.K., ROSKAMPFER U., RICKLI E.E.;
"Complete amino acid sequence of bovine plasminogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BERGLUND L., ANDERSEN M.D., PETERSEN TCloning and characterization of the Lnt. Dairy J. 5:593-603(1995).
                                  Tissue
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                         PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS50070; KRINGLE_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human plasminogen.";
Eur. J. Biochem. 149:267-278(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
Eutheria;
                                                                                    PFAM; PF00051; kringle; 5. PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 85023311.
MALINOWSKI D.P., SADLER J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLMN_BOVIN
                                                                       Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 706-812 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Characterization of a complementary deoxyribonucleic acid coding
                                                    remodeling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cetartiodactyla;
                                                    Serine protease; Plasma; Glycoprotein; Fibrinolysis; odeling; Blood coagulation; Kringle; Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
                                                                                                                                                                                                                                     CAA55939.1; -.
AAA30714.1; -.
                                                                                                                                                                                                      2PK4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Mammalia;
actyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAVIE E.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.E.;
bovine plasminogen cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               812
                                                  Kringle;
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Matches 2
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01-FEB-1991
15-JUL-1999
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ACT_SITE
ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                          O'REILLY M.S., HOLMGREN L., SHING Y., CHEN C., ROSENTHAL R. MOSES M., LANE W.S., CAO Y., SAGE E.H., FOLKMAN J.; "Angiostatin: a novel angiogenesis inhibitor that mediates suppression of metastases by a Lewis lung carcinoma."; Cell 79:315-328(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                     PLMN_MOUSE
P20918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chorda@a; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
            -
                                                                                                                                                                                                                                                          "Characterization of the cDNA coding for mous localization of the gene to mouse chromosome 3enomics 8:49-51(1990).
                                                                                                                                                                                                                                                                                         MEDLINE; 91184812.
DEGEN S.J., BELL S.M., SO
"Characterization of the
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                            PLASMINOGEN
                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                               CHARACTERIZATION OF ANGIOSTATIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 WEYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 VAVTESGHTCQRWSEQTPHKHNRTPENFPC-KNLEENYCRNPNGEKAPWC-YT-TNSEVR 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47
                                                                                    FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTEDUTIC FACTOR IN A VERIFITY OF OTHER PROCESSES INCLUDING EMERYONG DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, AS C1 AND YOU WILLEBRAND FACTOR.
ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND T
FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
                                        FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND METASTATIC TUMORS IN VIVO.

ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGYC
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Similarity 35.9%;
23; Conservative
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(Rel. 17,
(Rel. 38,
PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17, Created)
17, Last sequences 38, Last annotations
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Last annotation
(EC 3.4.21.7) [0]
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Pred. No. 1.05e-18;
Pred. '---+ches 27;
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KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
KRINGLE 5.
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CRC32;
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PROSITE: PS00134; TRYPSIN_HIS; 1.
PROSITE: PS00135; TRYPSIN_SER; 1.
PROSITE: PS50070; KRINGLE_2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A38514; A38514.
HSSP; P00747; 1PMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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    Local Similarity hes 24; Conser
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                                                                                                                                                                                                                                         SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EDE EUROPEAN BIOINFORMATICS. Institute. There are no restrictly non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVINVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAIN TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE SIMILARITY: CONTAINS 5 KRINGLE REGIONS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TRYPSIN FAMILY. BELONGS TO THE PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J04766; AAA50168.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease; Plasma; Glycoprotein; Fibri; odeling; Blood coagulation; Kringle; Zymogen;
                                                                731

731

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      Conservative
                                            AA;
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36.9%;
                                            90846
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Pred.
11; M
                                                    CATALYTIC
CHARGE RELAN
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CHARGE RELAN
BY SIMILARII
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KRINGLE 5.
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PLASMINOGEN LIGHT
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      Mismatches
              172; DB 1;
No. 2.80e-18;
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78)
78)
      Indels
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mogen; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary structure of guinea-pig Hageman factor: sequence around the cleavage site differs from the human molecule.";

RL Biochim. Biophys. Acta 1159:113-121(1992).

CC -!- FUNCTION: FACTOR XII IS A SERUM GLYCOPROTEIN THAT PARTICIPATES IN CENTRATION OF BRADYKININ AND ANGIOTENSIN.

CC -!- CATALYTIC ACTIVITY: CLEAVES SELECTIVELY ARG-|-ILE BONDS AND ACTIVATES COAGULATION FACTORS VII AND XI.

CC -!- CATALYTIC COUNTY: CLEAVES SELECTIVELY ARG-|-ILE BONDS AND ACTIVATES COAGULATION FACTORS VII AND XI.

COMPLEX BOUND TO AN ANIONIC SUFFACE. PREKALLIKREIN IS CLEAVED BY FACTOR XII TO FORM KALLIKREIN, WHICH THEN CLEAVES FACTOR XII FIRST TO ALPHA-FACTOR XIIA AND THEN TO BETA-FACTOR XIIA ALPHA-FACTOR XIIA ACTIVATES FACTOR XIIA AND THEN TO BETA-FACTOR XIIA. ALPHA-FACTOR XIIA.

-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-II DOMAIN.

-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-II DOMAIN.

-!- SIMILARITY: CONTAINS 1 KRINGLE REGION.

-!- SIMILARITY: CONTAINS 1 KRINGLE REGION.

-!- SIMILARITY: CONTAINS 1 KRINGLE REGION.

-!- SIMILARITY: CONTAINS 1 KRINGLE REGION.
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               PFAM; PF00008; EGF; 2.
PFAM; PF00039; fn1; 1.
PFAM; PF00040; fn2; 1.
PFAM; PF00051; kringle; 1.
PFAM; PF00089; trypsin; 1.
Glycoprotein; Blood coagulat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q04962;
01-FEB-1996 (Rel. 33
01-FEB-1996 (Rel. 33
01-MOV-1997 (Rel. 35
COAGULATION FACTOR )
                                                                                                                                                                           EMBL; X68615; CHSP; P00763; I
PROSITE; PS0002
PROSITE; PS0002
PROSITE; PS0002
PROSITE; PS0013
PROSITE; PS0118
PROSITE; PS0118
PROSITE; PS0118
PROSITE; PS0119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (Son send an email to license@isb-sib.ch).
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PS01186;
PS01253;
                                                                                                                                                                                                                                                                                  PS00022;
PS00023;
PS00134;
                                                                                                                                                                                PS50070;
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zoa; Chordata; Craniata; Vertebrata;
tia; Hystricognathi; Caviidae; Cavia
                                                                                                                                                                                                                           TRYPSIN_SER; 1.
EGF_2; 1.
                                                                                                                                                                                                                                                                             EGF_1; 2.
FIBRONECTIN_2;
TRYPSIN_HIS; 1.
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33, Last sequence update)
35, Last annotation update)
38 XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR)
                                                                                                                                                                                KRINGLE_2;
                                                                                                                                                                                                                                                                                                                                       KRINGLE_1;
EGF_1; 2.
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in; Blood coagulation; Plasma; Kringle; Fibrinolysis; EGF-like domain; Repeat;

Serine pi Zymogen;

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Best Local
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miniplasminogen.";
miniplasminogen.";
Eur. J. Biochem. 149:279-285(1985).
Eur. J. Biochem. 149:279-285 THE FIBRIN OF BLOOD CLOTS AND
-i- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND
A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCL
A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCL
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P06867;
01-JAN-1988
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Suina; Suidae; Sus.
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ACT_SITE
                                                                                                                                               SEQUENCE OF 450-790. MEDLINE; 85203907.
                                                                                                                                                                                                                               SCHALLER J., MARTI T.
"Amino acid sequence of the carbohydrate a
                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-560
                                                                                                                                                                                                                                                                                                                                                                01-JAR-1988 (Rel. 05, Created)
01-FBB-1991 (Rel. 17, Last sequence up
01-CCT-1996 (Rel. 34, Last annotation
PLASMINOGEN (EC 3.4.21.7).
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22; Conser
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                                                                                                            RICKLI E.E.;
complete amino-acid sequence
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12; |
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35C16971
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FIBRONECTIN TYPE-I.
EGF-LIKE 2.
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ALPHA-FACTOR XIIA LIGHT
FIBRONECTIN TYPE-II.
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1. No. 4.57e-
Mismatches
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1.57e-18
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plasmin. Comparison
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Best Local S
Matches 2
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PROSITE; PS00135; TRYPSIN_SER;
PROSITE; PS50070; KRINGLE_2; 5.
PFAM; PF00051; Kringle; 5.
PFAM; PF00089; trypsin; 1.
PFAM; PF00089; trypsin; 1.
PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                         FA12_BOVIN STAND

P98140;

01-FEB-1996 (Rel. 33

01-FEB-1996 (Rel. 33

01-NOV-1997 (Rel. 35

COAGULATION FACTOR X

(HAF) (FRAGMENT).
MEDLINE: 94242782.

MEDLINE: 94242782.

SHIBUYA Y., SEMBA U., OKABE H., KAMBARA T., YAMAMOTO T.;

"Primary structure of bovine Hageman factor (blood coagulation XII): comparison with human and guinea pig molecules.";

Riochim. Biophys. Acta 1206:83-70(1994).
                                                                                                                                                                                Eutheria;
Bovinae; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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CARBOHYD
SEQUENCE
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PIR; S037
HSSP; P00
PROSITE;
PROSITE;
PROSITE;
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                                                                                                                       TISSUE=LIVER;
                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                         SEQUENCE FROM N.A.
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ENZYME REGULATION: CONTRETED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
SIMILARITY: CONTAINS 5 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PEPTIDASE FRANILY SI; ALSO KNOWN AS THE SIMILARITY: BELONGS TO PEPTIDASE FRANILY SI; ALSO KNOWN AS THE SIMILARITY: BELONGS TO PEPTIDASE FRANILY SI; ALSO KNOWN AS THE PROMOTER AND THE PROPERTY OF THE PARAMETER AND THE PROPERTY OF THE PARAMETER AND THE PARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGYC
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S03733; S03733.
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24; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                            33, Created)
33, Last sequence update)
35, Last annotation update)
R XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR)
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TRYPSIN_SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRYPSIN_HIS;
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                                                                                                                                                                                                    Ruminantia;
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Pred. No. 4.57e-18
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KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
KRINGLE 5.
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CHARGE RELA
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LIGHT CHAIN B.
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RELAY
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                                                                                                                                                                                                    Pecora;
                                                                                                                                                                                                  Vertebrata; Mamm
Pecora; Bovoidea;
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Y SYSTEM.
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PEAM; PF00008; EGF; 2.

PFAM; PF00008; EGF; 2.

DR PFAM; PF00039; fnl; 1.

DR PFAM; PF00051; kringle; 1.

PFAM; PF00051; kringle; 1.

PFAM; PF00089; trypsin; 1.

Glycoprotein; Blood coaquifydrolase; Fibrinolycestronau
  CCCCCCCCCCRRRRRRR
                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00022; EGF_1; 2.1.
PROSITE; PS00023; FIBRONECTIN_2; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS01136; EGF_2; FALSE_NEG.
PROSITE; PS01233; FIBRONECTIN_1; 1.
PROSITE; PS01233; FIBRONECTIN_1; 1.
PROSITE; PS01253; FIBRONECTIN_1; 1.
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between
the Euro
use by
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-! CATALYTIC ACTIVITY: CLEAVES SELECTIVELY ARG-|-ILE BONDS AND ACTIVATES COAGULATION FACTORS VII AND XI.
-! PTM: O- AND N-GLYCOSYLATED (BY SIMILARITY).

-! MISCELANBEOUS: FACTOR XII, PRERALLIKREIN, AND HAW KININOGEN FORM A COMPLEX BOUND TO AN ANIONIC SURFACE. PREKALLIKREIN IS CLEAVED BY FACTOR XII TO FORM KALLIKREIN, WHICH THEN CLEAVES FACTOR XII FIRST TO ALPHA-FACTOR XIIA AND THEN TO BETA-FACTOR XIIA ALPHA-FACTOR XII TO FACTOR XII A SETA-FACTOR XIIA ACTIVATES FACTOR XI TO FACTOR XIIA AND THEN TO BETA-FACTOR XII SIALPHA-FACTOR XII AS IT LACKS THE TRYPSIN/ KALLIKREIN CLEAVEGE SITE.

- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-II DOMAIN.
- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-II DOMAIN.
- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY:

- TRYPSIN FAMILY.
                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                        CHAIN
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entities
                                                                                                                                                                                   DOMAIN
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-:- FUNCTION: FACTOR XII IS A S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 10-21;
MEDLINE; 77182112.
FUJIKAWA K., WALSH
                                                                                                                                                         DOMAIN
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                               DOMAIN
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PROSITE; PS00021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S70164; AAB30804.1; -. P00763; 1DPO.
  WALSH A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRINGLE_1; 1.
EGF_1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350-364 AND 525-550
                                                                                                                                                                                                                                                                                                                          coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAVIE W.E.; ization of bovine
                                                                                                                                                                                                                                                                                                             EGF-like
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
BY SIMILARITY .
                                                                                                                                                                     KRINGLE.
PRO-RICH.
                                                                                                                                                                                                                                     ALPHA-FACTOR XIIA HEAVY
ALPHA-FACTOR XIIA LIGHT
FIBRONECTIN TYPE-II.
                                                                                                                                                         CATALYTIC
                                                                                                                                                                                                 FIBRONECTIN EGF-LIKE 2.
                                                                                                                                                                                                                            EGF-LIKE
                                                                                                                                                                                                                                                                                                           Plasma; Kringle;
e domain; Repeat;
                                                                                                                                                                                                               TYPE-I
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, (BX
, XB)
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                                                                                                                                                                                                                                                                                                             Serine protease;
Zymogen; Signal.
                                                                                                            Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration -
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Matches 2
                                                                                                                                                                             "THE STRUCTURE OF THE TATA-LESS rat tissue-type plasminogen activator The Structure of the TATA-LESS rat tissue-type plasminogen activator gene. Species-specific sequence divergences in the promoter predict differences in regulation of gene expression.";

J. Biol. Chem. 265:2022-2027(1990).

-i- FUNCTION: TPA CONVERTS PLASMINOGEN TO PLASMIN BY HYDROLYZING AND SINGLE R-V BOND IN PLASMINOGEN. ACTIVE IN TISSUE REMODELING AND DESTRUCTION, PARTICULARLY IN FIBRINOLYSIS, AND IN CELL MIGRATION.

-I- CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-I-VAL BOND IN PLASMINOGEN TO FORM PLASMIN.

-I- MISCELLANDOUS: TPA ATTACHES TO THE KRINGLE STRUCTURE OF THE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
       This SWISS-PROT entry is copyright. It is p between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                        cioning and characterization of plasminogen activator.";
DNA 7:671-677(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OROT_RAT STANDARD; PRT; 559 AA P19637; O1-FEB-1991 (Rel. 17, Created) O1-NOV-1991 (Rel. 20, Last sequence update) O1-NOV-1997 (Rel. 35, Last annotation updat TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC T-PLASMINOGEN ACTIVATOR).
                                                                                                                     ----
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 90130448.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A MEDLINE; 89170114
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                     SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 2
SIMILARITY: BELONGS TO
                                                                                                           TRYPSIN FAMILY.
                                                                                                                                                                       CHAIN OF FIBRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
23; Conse
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230
258
336
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                                                                                                                     EGF-LIKE DOMAIN.
FIBRONECTIN TYPE-I DOMAIN
KRINGLE REGIONS.
PEPTIDASE FAMILY S1; ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 169;
Pred. No. 1.
12; Mismatc
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                                                                    ght. It is produced through Bioinformatics and the EN
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R (EC 3.4.21.
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                                                                                                                                                                                                                                                                                                                                                                                 rat tissue-type
                                                                                                                      S1; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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Rattus.
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PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS001035; EGF_1; 1.
PROSITE; PS01106; EGF_2; 1.
PROSITE; PS01123; FIBRONECTIN_1; 1
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS00021; KRINGLE_2; 2.
PROSITE; PS00003; EGF; 1.
PROMITE; PS00039; fn1; 1.
PFAM; PF000039; trypsin; 1.
PFAM; PF000089; trypsin; 1.
PFAM; PF000089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A31597; A31597; A31597; A31597; A31597; A35029; A35029; A35029; A35029; A35029; A35029; A35023; PROSSITE; PS00134; TIP PROSSITE; PS00135; TIP PROSSITE; PS00022; E0
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                       Plasma; Kringle; EGF-like
SIGNAL 1 17
                                                                                                                                                                                                                                                                                                                                                                                                        Plasminogen
                  232
54
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L; M31195; AAA422
L; M31196; AAA422
L; A19618; CAA014
; A1967; A31597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A35029; A35029.
APCIRWAEVPPFLERSPPASWA--QLRGQ-RHNFCRSPDGAGRPWCFYGDARGKVDWGYC
                ASCLPWNSMI-LIGKTYTAWRANSQALGLGRHNYCRNPDGDAKPWCHVMKDR-KLTWEYC 289
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M31197;
M31185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    м31193;
                                    similarity 41.0%;
25; Conservative
                                                                       481
380
559
                                                                                                                                                                                                                                                                                                                                                                                                       activation;
                                                                                                                                         309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA42261.1;
AAA42261.1;
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AAA42261.1;
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380
62903
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308
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                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase;
                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED
                                                                                                                                                                                                                                                                                                                                                                                               domain;
                                    Pred.
12; N
                                                                                                                                                                CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                            Score 164; DB 1;
Pred. No. 1.38e-16;
                                                                                                  BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY.
BY SIMILARITY.
                                                                                 POTENTIAL.
E -> K (IN
                                                                                                                                                                                                                                                                                                  KRINGLE
KRINGLE
                                                                                                                                                                                                                                                                                                                                       TISSUE PLASMINOGEN ACTIVATOR B CHAIN (LIGHT, SERINE PROTEASE).
                                                                                                                                                                                                                                                                                                                                                                  TISSUE PLASMINOGEN ACTIVATOR
                                                                                                                                                                                                                                                                                                                                                                                     lain; Signal.
PROBABLE.
                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-I.
                                                                         -> K (IN
A106A89E
                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease;
                                                                        REF. 1).
                                                                                                                                                          SIMILARITY).
                                    19;
                                                      Length 559
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                 A CHAIN
                                    <u>ა</u>
                                    Gaps
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RESULT RESULT REPORT RESULT REPORT RESULT REPORT RESULT REPORT REPORT RESULT REPORT RE
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P SIGNAL SEQUENCE CLEAVALL

XX MEDLINE; 91207365.

RA YOSHIYAMA Y., ARAKAKAI N., NAKA D., TAKAHASIL.

RA NAKAYAMA H., GOHDA E., KITAMURA N., TSUBOUCHI H., ISHLL.

RA HISHIDA T., DAIKUHARA Y.;

RI "Identification of the N-terminal residue of the heavy chain of the N-tive and recombinant human hepatocyte growth factor.";

**Tive and recombinant human hepatocyte growth factor.";

**Tive and recombinant human hepatocyte growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
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P14210;
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 91334393.
WEIDNER K.M., ARAKAKI N., HARTMANN G.,
RIEDER H., FONATSCH C., TSUBOUCHI H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HEPATCOYTE GROWTH FACTOR PRECURSOR (SCATTER F.
(HEPATOPOEITIN A).
                                                                                                                                                                                                                                                                                                                            "Evidence for the identity of human "Evidence for the factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAKAMURA T., NISHIZAWA T., HAGIYA M., SUGIMURA A., TASHIRO K., SHIMIZU S.; "MOLBEULAR cloning and expression of Pature 342:440-443(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and expression of cDNA for dilletent... growth factor from human leukocyte."; growth factor from human 172:321-327(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-LEUKOCYTE;
MEDLINE; 91025062.
SEKI T., IHARA I., SUGIMURA A., SHIMONISHI M., NISHIZAWA T.,
SEKI T., HARA I., SUGIMURA T., SHIMIZU S.;
ASAMI O., HAGIYA M., NAKAMURA T., SHIMIZU S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and
growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 89392017.
MIYAZAWA K., TSUBOUCHI H., NAKA D., TAKAHASHI
ARAKAKI N., NAKAYAMA H., HIRONO S., SAKIYAMA C
GOHDA E., DAIKUHARA Y., KITAMURA N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE: 91340155.
SEKI T., HAGIYA M., SHI
"Organization of the hu
Gene 102:213-219(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Ci
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                        hepatocyte growth
Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-EMBRYONIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIBROBLAST;
                                                                                                                                                                                                                                                                                                        factor.";
Sci. U.S.A. 88:7001-7005(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHIMONISHI M., NAKAMURA 's human hepatocyte growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Ve: Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Commun.
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                                                                                                                                                                                                                                                                                                                                                         scatter
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ZHOU H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ULTSCH M., LOKKER N.A., GODOWSKI P.J., "Crystal structure of the NXI fragment factor at 2.0-A resolution"; Structure 6:1383-1393(1998).
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BAKER J.B., GODOWSKI P.J.;
"Structure-function analysis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZHOU H., MAZZULLA M.J., KAUFMAN J.D., STAHL S.J. RUBIN J.S., BOTTARO D.P., BYRD R.A.;
The solution structure of the N-terminal domain actor reveals a potential heparin-binding site.
Structure 6:109-116(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 31-127. MEDLINE; 98154323.
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NAKAMURA T., SHIMIZU
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                ; JH0579; JH0579.
; S06794; S06794.
; 2HGF; 24-JUN-98.
; 1BHT; 18-NOV-98.
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SUBBURIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY
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S.;
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01-NOV-1995 (Rel. 32, Last annotation updat
HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECU
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HAN S., STUART L.A.,
"Characterization of
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Homo sapiens (Human)
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MIM; 142408:
PROSITE; PS00021; KRINGLE_1; 4
PROSITE; PS00070; KRINGLE_2; 4
PFAM; PF00051; kringle; 4.
PFAM; PF00089; trypsin; 1.
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-i- FUNCTION: PROBABLY HAS NO PROTEOL CHARACTERISTIC OF SERINE PROTEASE
                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                       CARBOHYD
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EMBL; U37055; AAC504
PIR; A40331; A40331.
301 GVPCQRWDAQIPHQHRFTPEKYAC-KDLRENFCRNPDGSEAPWCF
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRYPSIN FAMILY. BELONGS TO THE PLASMINOGEN
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U37055; AAC50471.1;
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                                                                                                                /FTId=VAR_006632.
C9978F05 CRC32;
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                                                                                                                                                                                                                POTENTIAL.
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                                      Mismatches
                                                     161; DB 1;
No. 5.86e-16;
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DOMAIN
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CARBOHYD

Signal; SIGNAL CHAIN

Growth PFAM; PF00051; PFAM; PF00089;

Alternative ⊥ 33 496 33

HEPATOCYTE GROWTH FACTOR ALPHA HEPATOCYTE GROWTH FACTOR BETA C PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).

trypsin; Kringle; kringle;

Glycoprotein; Serine

protease homolog;

SIMILARITY

CHAIN

MOD_RES

DOMAIN DOMAIN DOMAIN

DOMAIN

33 129 212 306 392 496 488 488 488 403 569

128 207 207 289 4470 97 97 85 6569

PAP

KRINGLE 1.

KRINGLE 2.

KRINGLE 3.

KRINGLE 4.

SERINE PROTEASE-LIKE.

BY SIMILARITY.

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EMBL; D10213; BAA01065.1; -.
HSSP; D14210; 2HGF.
MGD; MGI:96079; HGF.
PROSITE; PS00021; KRINGLE_1; 4
PROSITE; PS50070; KRINGLE_2; 4
                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SASAKI M., NISHIO M., SASAKI T., ENAMI J.;
"Identification of mouse mammary fibroblast-derived mammary growth factor as hepatocyte growth factor.";
Biochem. Biophys. Res. Commun. 199:772-779(1994).
-!- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES IT HAS NO DETECTABLE PROTEASE ACTIVITY.
-!- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGF_MOUSE STANDARD; PRT; 728 AA. Q08048; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER (HEPATOPOEITIN A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LONG FORM.
SIMILARITY: CONTAINS 4 KRINGLE REGIONS
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
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ALTERNATIVE PRODUCTS: A SI
ALTERNATIVE RNA SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOW TRYPSIN FAMILY. BELONGS TO THE PLASMINOGEN SUBFAMILY.
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Sciurognathi; Muridae;
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ae; Murinae;
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Tabular output not generated. Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Mon Mar 13 10:21:30 2000; MasPar time 14.19 Seconds 356.626 Million cell updates/sec ************

(MT)

Description:
Perfect Score:
Sequence:

Title: >US-09-147-947-6 (40-112) from US09147947A.pep (2 of 6) 611

1 CPAGEPWVSVTDFGAPCLRW......RPWCFYGDARGKVDWGYCDC 73

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 37.029; Variance 62.983; scale 0.588

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ĬĎ	Description	Pred. No.
Ð	207	33.9	946	13	Q07153	RECEPTOR TYROSINE KINA	3.09e-24
N	188	30.8	597	11			3.03e-20
ω	173		716	11	P70521	HEPATOCYTE GROWTH FACT	3.72e-17
4	167	27.3	560	4	Q14520		6.13e-16
ъ	165	27.0	616	σ	097507	FXII.	1.55e-15
0	163	26.7	290	4	Q02935	HEPATOCYTE GROWTH FACT	3.92e-15
7	163	26.7	296	4	Q14519		.92e-1
œ	162	26.5	2869	δ	Q28398	APOLIPOPROTEIN (FRAGME	
9	161	26.4	567	4	Q13208	HEPATOCYTE GROWTH FACT	9.86e-15
10	161	26.4	711	4	Q14870	MACROPHAGE-STIMULATING	9.86e-15
11	161	26.4	728	11	Q64007	HEPATOCYTE GROWTH FACT	9.86e-15
12	161	26.4	748	11	Q61662	HEPATOCYTE GROWTH FACT	9.86e-15
13	160	26.2	806	o	018783	PLASMINOGEN.	1.56e-14
14	159	26.0	710	13	Q91402	HEPATOCYTE GROWTH FACT	2.47e-14
15	152	24.9	454	σ	046506	APOLIPOPROTEIN A (FRAG	6.02e-13
16	150	24.5	717	13	P70006	HEPATOCYTE GROWTH FACT	1.49e-12
17	149	24.4	215	13	042341	HGF ALPHA-CHAIN (FRAGM	2.34e-12
18	149	24.4	726	13	Q90978	HEPATOCYTE GROWTH FACT	2.34e-12
19	147	24.1	704	13	Q90865	HEPATOCYTE GROWTH FACT	5.74e-12
20	147	24.1	810	4	Q15146	PLASMINOGEN PRECURSOR.	5.74e-12

Uschit 1, maybe

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	
90	91	93	93	111	111	115	116	116	116	116	116	119	122	123	124	127	128	135	135	138	138	138	140	141	
14.7						18.8	19.0	19.0	19.0	19.0	19.0	19.5	20.0			20.8			22.1	22.6	•				
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Q91001	Q90504	8ASX6Ö	097887	Q25101	000318	Q01973	Q01974	Q9Z139	Q17576		077688	Q28911	055027	Q9XT70	Q13494	Q9Z138	Q90675	096391	002001	Q16618	Q15844	046507	Q16609	Q91691	
THROMBIN.	THROMBIN.	SCO-SPONDIN (FRAGMENT)	REISSNER'S FIBER GLYCO	SERINE PROTEINASE.	PUTATIVE PROTEIN.	PROTEIN-TYROSINE KINAS	PROTEIN-TYROSINE KINAS	ROR1.	KIN-8 PROTEIN.	NEUROTROPHIC RECEPTOR	PROTHROMBIN PRECURSOR	APOLIPOPROTEIN A (FRAG	HEPATOCYTE GROWTH FACT	UROKINASE-TYPE PLASMIN	HGF AGONIST/ANTAGONIST	ROR2	TISSUE-TYPE PLASMINOGE	RECEPTOR TYROSINE KINA	NEUROSPECIFIC RECEPTOR	UROKINASE PRECURSOR (E	UROKINASE-TYPE PLASMIN	PLASMINOGEN (FRAGMENT)	(APOARGC).	GROWTH FACTOR LIVERTIN	
9.52e-02		3.16e-02	.166	. 90e	.90e-	7e-	.76e	3.76e-06	3.76e-06	3.76e-06	3.76e-06				1.32e-07		ው	.17e-	.17e-	.13e-1	.13e-			8.33e-11	

ALIGNMENTS

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SULT 03572	106 DWGYCD	5 533 RWEFCN 538	47 VSVTDFGAPCLRWAEVPPFLERSPPASWAQLRGQRHNECRSPDGAG-RPWCFYGDARGKV 105	476 VNVTASGISCORWSEQAPHFHRRLPEIFPEL-ANSD	Query Match 33.9%; Score 207; DB 13; Length 946; Best Local Similarity 39.4%; Pred. No. 3.09e-24; Matches 26; Conservative. 13; Mismatches 23; Indels 4; Gaps	SEQUENCE	R PRINTS; PRO0109; TYRKINASE.	THAM; PROCOSE; KI	PFAM; PF00069;	PFAM; PF00047; ig; 3.	PROSITE; PS00109;	PROSITE: PS00107; PROTEIN KINASE ATP;		Proc. Natl. Acad. Sci. U.S.A. 90:2895-2899(1993).	distinct class of receptor tyrosine kinases."						[1]	Elasmobranchii; Rajiformes; Torpedinoidei; Torpedini	Eukaryota; Metazoa;	Torpedo californica	RECEPTOR TYROSINE KINASE	01-NOV-1999 (TrEMBLrel. 12, Last	01-NOV-1996 (TrEMBLIE) 01.	01-NOV-1996 (TrEMBITE)	007153	TD 007153 PRELIMINARY: PRT: 946 AA	

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RESULT
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AC P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                             EMBL; X95096; CAA64473.1; -. HSSP; P00747; lpwK.
PFAM; PF00051; kringle; 4.
PFAM; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00040; fn2; 1.
PFAM; PF00089; trypsin; 1.
FAM; PF00051; kringle; 1.
FAM; PF00008; EGF; 2.
PFAM; PF000039; fn1; 1.
PFANTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00712; KRINGLE.
PRINTS; PR00918; KRINGLE.
SEQUENCE 597 AA; 65638 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      035727;
01-JAN-1998 (TrEMBLrel. (
01-JAN-1998 (TrEMBLrel. (
01-NOV-1999 (TrEMBLrel. FACTOR XII.
PRINTS; PRO0018;
PRINTS; PRO0722;
Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 227:273-280(1996).
-!- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CHARACTERISIC OF SERINE PROTEASES CATALYTIC SITES ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P70521 PRELIMINARY; PRT; 716 AA.
P70521;
P10521;
P10521;
P10521;
P10521;
P10521;
P10521;
P10522;
P1052
                                                                                                                                                                                          CONSERVED.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
TRYPSIN FAMILY. BELONGS TO THE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                          OHSHIRO K., IWAMA A., MATSUNO K., TEKASU N., SUDA T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER;
MEDLINE; 9701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamm
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                        "wolecular cloning of rat macrophage-stimulating involvement in the male reproductive system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00023; FIBRONECTIN_2; PROSITE; PS01253; FIBRONECTIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1996) to the EMBL; x99571; CAA67891.1; HSSP; P00760; 1AQ7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHLOESSER M., SCHWAGER S., ENGEL W.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        μtheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 DWGYC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWDYC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVTDFGAPCLRWAEVPPFLERSP-PA-SWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                          97011126.
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llarity 40.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
  3
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12,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 188; DB 11;
Pred. No. 3.03e-20;
13; Mismatches 20;
  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1EA8CD44 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                 EZAKI T.,
                                                                                                                                                                                                                                                                                                                                                                                                                    SAKAMOTO
                                                                                                                                                                                             SUBFAMILY
                                                                                                                                                                                                                      ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 597;
                                                                                                                                                                                                                                                                                                                                                                 protein
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Best Local S
Matches 1
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Best Local Similarity
Matches 22; Consei
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Q14520; 000663;
01-NOV-1996 (TIEMBLIEL 01, C
01-NOV-1996 (TIEMBLIEL 12, I
01-NOV-1999 (TIEMBLIEL 12, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D49742; BAA08576.1; -...
EMBL; S83182; AAB46909.1; -...
HSSP; P00763; 1DPO.
PFAM; PF00008; EGF; 3.
PFAM; PF000081; kringle; 1.
PFAM; PF000089; trypsin; 1.
PFAN; PF00018; KRINGLE.
PRINTS; PR00012; CHYMOTREPSIN.
SEQUENCE 560 AA; 62671 MW; 4
                                                                                                                                                                          097507
097507;
01-MAY-1999
01-MAY-1999
01-NOV-1999
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SEQUENCE
                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                  SEQUENCE FROM N.A.
TISSUE=LIVER;
                                                                                                                                                        FXII.
TAKAHASHI T., KIHARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biochem. 119:1157-1165(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96425001.
CHOI-MIURA N.H., TOBE T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGF ACTIVATOR LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein (PHBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. KITAMURA N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein (PHBP) from human plasma: it has three EGF, a kring serine protease domain, similar to hepatocyte growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMITA M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                     243 HNFCRNPDADEKPWCFIKVTNDKVKWEYCD 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 VDVTESGRECORWDLQHPHSHPFHPEKFPD-KALKDNYCRNPDASERPWCYTTDP--NVE 259
                                                                                                                                                                                                                                                                                                                                                            82
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                                                                                                                                                                                                                                                                                                                                                            HNFCRSPDGAGRPWCFYGDARGKVDWGYCD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : :||
WGYCD 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.3%;
Similarity 56.7%;
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716 AA;
                                                                                                                                                                          (TrEMBLrel.)
(TrEMBLrel.)
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                                                                                                                                                                                                                                                                  PRELIMINARY;
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larity 33.8%;
Conservative
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80733
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                                                                                                                                                                          Created)
Last sequence
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 173; DB 1
Pred. No. 3.72e-
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 167; DB 4, pred. No. 6.13e-16;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4AC81907 CRC32;
                                                                                                                                                                          sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173; DB 11;
No. 3.72e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of a
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                                                                                                                                                                                                                                                                    616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANO Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAZDA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                        Query Match
Best Local S
Matches 2
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Best Local S
Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02935
002935;
002935;
01-NOV-1996
01-NOV-1999
                                                                                                                                                                                                 Growth
SIGNAL
                                                                                                                                                                                                                                                                                "A functional domain in the heavy chain of scatter factor/hepatocyte growth factor binds the c-Met receptor and induces cell dissociation but not mitogenesis.";

Proc. Natl. Acad. Sci. U.S.A. 89:11574-11578(1992).

-!- FUNCTION: HOF IS A POTENT MITOGEN FOR ADTURE PARENCHYMAL—
HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS A GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES. IT HAS NO DETECTABLE PROTEASE ACTIVITY.

-!- SIMILARRIY: HIGH, TO OTHER HGF; LOWER, TO PLASMINOGEN.

EMBL, X57574; CAA4082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGF.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata;
Eukaryota; Primates; Catarrhini; Hominida
                                                                                                                SEQUENCE
                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Porcine liver factor XII.";
Submitted (JAN-1999) to the EMBL/GenBank
EMBL; AB022426; BAA37148.1; -.
HSSP; P00763; IDPO.
PROSITE; PS00023; FIBRONECTIN_2; 1.
PROSITE; PS01253; FIBRONECTIN_1; 1.
SEQUENCE 616 AA; 68012 MW; 31CCD856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01.NOV-1996 (TIEMBLIEL. 01, Created)
01.NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01.NOV-1999 (TIEMBLIEL. 12, Last annotation update)
01.NOV-1999 (TIEMBLIEL. 12, Last annotation update)
HEPATOCYTE GROWTH FACTOR, HEAVY CHAIN PRECURSOR.
                                                                                                                                                                                                                             PFAM; PF00051; kringle; 2. PRINTS; PR00018; KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "An alternatively processed mRNA growth factor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 91200041.
MIYAZAWA K., KITAMURA A., NAKA D., KITAMURA N.;
                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMOGLIO P.M., BIRDMEIER W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HARTMANN G., NALDINI L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Biochem. 197:15-22(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISSUE=PLACENTA;
                            226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 GAPCQPWASEATYWNMTAEQALNWG-L-GD-HAFCRNPDNDTRPWCFVWRG-DQLSWQYC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.0%;
Local Similarity 40.0%;
wes 24; Conservation
 50
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                          TESGKICQRWDHQTPHRHKFLPERYPD-KGFDDNYCRNPDGQPRPWCYTLDPHTR--WEY 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAPCLRWAEVPPFLERSP-PA-SWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVDWGYC 110
IDEGAPCLRWAEVPPELERSPPASWAQLRGQRHNECRSPDGAGRPWCFYGDARGKVDWGY 109
                                                                                                                                                                                                                                                                         L02931;
                                                                                                                                                                                                  factor; Kringle; Signal
1 31 Po
                                                         Similarity 22; Conse
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1BHT.
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206
288
32
                                                                     26.7%;
                                                                                                                33765 MW;
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                                                                                                          KRINGLE 1 (BY SIMILARITY).
KRINGLE 2 (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
W; 9EF113DE CRC32;
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Pred. No. 1.55e-15;
                                                        11;
                                                                   Score 163; DB 4;
Pred. No. 3.92e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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RESULT 7
ID Q14519;
AC Q14519;
AC Q14519;
AC Q14519;
AC Q14519;
DT 01-NOV-1996 (TIEMBLEG! 01, C;
DT 01-NOV-1996 (TEMBLEG! 12, L;
DT 01-NOV-1996 (TEMBLEG! 12, L;
DT 01-NOV-1996 (TEMBLEG! 12, L;
DE COMPETITIVE HGF ANTAGONIST
OS Homo sapiens (Human).
OC Eutharia; primates; Catarrhin.
RN [1]
RP SEQUENCE FROM N.A.
RA CHAN A.M.L., RUBIN J.S., BOTTY
RA ARRONSON S.A.;
RI Science 0.0-0(0).
DR EMBL; M77227; AAA35980.1; -.
DR HSSP; P14210; 1BHT.
DR PFAM; PF00051; KrINGLE.
SQ SEQUENCE 296 AA; 34546 MW;
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IDT AC Q2

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Best Local
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Q28398;
Q1-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-NOV-1999 (TREMBLrel. 12, L
APOLIPOPROTEIN (FRAGMENT).
                           EMBL; U33170; AAC48522.3
HSSP; P00747; 1PMK.
PFAM; PF00051; kringle;
                                                                                                                                                                                                                                                                                                                                       LAWN R.M., BOONMARK N.W., SCHWARTZ K., LIND:
BYRNE C.D., FONG K.J., MEER K., PATTHY L.;
"The recurring evolution of lipoprotein(a).
hedgehog apolipoprotein(a).";
hedgehog apolipoprotein(a).";
J. Biol. Chem. 270:24004-24009(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erinaceus europaeus (Western European hedgehog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96025778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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VSVTDFGAPCLRWAEVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVD 106
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                                                                                                Similarity 23; Conser
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                                                                                                                                                                                                2869 AA;
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larity 36.1%;
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Pred. No. 3.92e-15;
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                                                                                                                         6.22e-15;
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                                                                                               Query Match
Best Local S
Matches 2
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Q14870
Q14870;
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                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM: PEO0051; kringle: 4.
PEAM: PE00089; trypsin; 1.
PRINTS: PR00018; KRINGLE.
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                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MBL; U28054; AAC63092.1; -. MSSP; P00747; 2PK4.
PFAM; PF00051; KTINGLE: 4.
PRINTS; PR00018; KRINGLE.
SEQUENCE 567 AA; 64116 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSHIMURA T., YUHKI N., WANG M.H., SKEEL A., LEC Cloning, Sequencing, and expression of human maprotein (MSP, MST1) confirms MSP as a member of proteins and locates the MSP gene on chromosome J. Biol. Chem. 268:1546-15468(1993).

EMBL: L11942; AAA59872.1; -.
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01-NOV-1996 (TremBlrel.
01-NOV-1999 (TremBlrel.
MACROPHAGE-STIMULATING F
                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEGEN S.J.F., MCDOWELL S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2474 WEYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
301 GVPCQRWDAQIPHQHRFTPEKYAC-KDLRENFCRNPDGSEAPWCF 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 93340141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 GVPCQRWDAQIPHQHRFTPEKYAC-KDLRENFCRNPDGSEAPWCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ubmitted (MAY-1995) to the
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                                                                                               Similarity
21; Conse
                                                                                                                                                                                                                                                                                                                                                                                    PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
21; Conse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2477
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19
484
711 AA;
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                                                                                                  Conservative
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483
711
80353 .
                                                                                                                             26.4%;
46.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 01, Created)
. 01, Last sequence update)
. 12, Last annotation update)
PROTEIN PRECURSOR.
                                                                                                                                                                                                                            WW;
                                                                                                                                                                                               POTENTIAL.
MACROPHAGE-STIMULATING P
MACROPHAGE-STIMULATING P
MACROPHAGE-STIMULATING F
1445C010 CRC32;
                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 161; DB 4;
Pred. No. 9.86e-15;
3; Mismatches 20
                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
l; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2A95547
                                                                                            re 161; DB 4
1. NO. 9.86e-
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711
                                                                                                                         DB 4;
.86e-15;
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                                                                                                                                                                                                                                                       PROTEIN.
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                                                                                                                                                              711;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of kringle
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Best Local S
Matches 2
Query Match
Best Local Similarity
Matches 22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                   factor gene.";

Cell Adhes. Commun. 1:101-111(19
EMBL; S71816; AAB31855.1; -...
HSSP; P14210; 1BHT.
MGD; MGI:96079; Hgf.
PFAM; PF00051; kringle; 4.
PFAM; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
SEQUENCE 728 AA; 82972 MW; E
                                                                                                                                                                                                                                      Q61662;
Q61662;
Q1-NOV-1996
Q1-NOV-1996
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Q64007;
01-NOV-1996
01-NOV-1996
01-NOV-1999
                                                                              MGD;
                                                                                                                                                      [1]
SEQUENCE FROM N.A.
STN=R6SJLF1/J; TISSUE=LIVER;
                                                                                                                                                                              nus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eurtheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                        PFAM; PF00051; kringle; PFAM; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGF.
Mus musculus (Mouse).
Mus musculus (Mouse).
                                       SEQUENCE
                                                                                      EMBL; X72307; CAA51054.1;
HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGF
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                                                  NON_TER
                                                                                                           Biochim. Biophys. Acta 1216:299-303(1993).
                                                                                                                                         LIU
                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                               HEPATOCYTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                   Molecular cloning and characterization of nepatocyte growth factor.";
                                                                                                                                                                                                                                                                                                                     110
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                                                                                                                                                                                                                                                                                                                                                           50
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                                                                             MGI:96079; Hgf.
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                                                                                                                                                                                                                                                                                                                                       284
                                                                                                                                      MICHALOPOULOS G.K., ZARNEGAR R.;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
22; Conser
                                                                                                                                                   94060105.
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Rodentia;
                                                                                                                                                                                                                             96 (TremBLrel. 01, 0
96 (TremBLrel. 01, 1
99 (TremBLrel. 12, 1
99 (FROWTH FACTOR (FR
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                                       748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic
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 26.4%;
larity 36.1%;
Conservative
                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                       AA;
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                                       85200
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01,
12,
                                                                                                                                                                                                                              (FRAGMENT).
                                       MW;
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Score 161; DB 11;
Pred. No. 9.86e-15;
10; Mismatches 26
                                                                                                                                                                                                                                       Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                        Score 161;
Pred. No. 9.
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Last annotation updat
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thi; Muridae;
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                                       24AE0820 CRC32;
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).86e-15;
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ae; Murinae;
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                   Length 748;
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TDFGAPCLRWAEVPPFLERSPPASWAQLRGQRHNFCRSPDGAGRPWCFYGDARGKVDWGY 109 TESGKTCQRWDQQTPHRHKFLPERYPD-KGFDDNYCRNPDGKPRPWCYTLDP-DT-PWEY

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RESULT
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Best Local Similarity 32.3%;
   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AKU1227;
HSSP; P00747; 5HPG.
PFAM; PF00051; Kringle; 5.
PFAM; PF00089; Trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
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01-JAN-1998
01-NOV-1999
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018783;
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1931402;
191402;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HEPATOCYTE GROWTH GROWTH FRAGMENT).
                                                                                                                                                                                                           MEDLINE; 95267690.

NAKAMURA H., TASHIRO K., NAKAMURA T., SHIOKAWA MAKAMURA T., TASHIRO K., NAKAMURA T., SHIOKAWA "MAKAMURA T. CONING OF XENDRUS HGF CDNA and its Yengris early embryogenesis.";

Yengris early embryogenesis.";

Yengris early embryogenesis.";

EMBL: 57422; ABB43454.1;

EMBL: 57422; ABB43544.1;

EMBL: 57422; ABB43544.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacropus eugenii (Tammar wallaby).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                       PFAM; PF00051; kringle; 4. PFAM; PF00089; trypsin; 1. NON_TER 710 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 ISKTESGIECQPWDSQEPHSHEYIPSKFPS-KDLKENYCRNPDGEPRPWCFTSNP-EKR- 253
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Similarity
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   26.0%;
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   Score 159; DB 13; Pred. No. 2.47e-14;
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Xenopodinae;
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COX L.A., JETT C., HIXSON J.E.;
COX L.A. (CCT-1997) to the EMBL,
Submitted (CCT-1997) to the EMBL,
EMBL; AF029691; AAB97886.1; -.
HSSP; P00747; ZPK4.
PFAM; PF00051; kringle; 2.
PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                      046506; PRELIMINARY; PRT; 454 AA. 046506; O1-JUN-1998 (TrEMBLrel. 06, Created) O1-JUN-1998 (TrEMBLrel. 12, Last sequence update) O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                           Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
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NON_TER
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llarity 33.9%;
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Pred. No. 6.02e-13;
12; Mismatches 24;
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

dd_u protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Mon Mar 13 10:19:31 2000; MasPar time 8.11 Seconds 391.512 Million cell updates/sec

Sequence: Description: Perfect Score: Title: >US-09-147-947-6 (578-822) from US09147947A.pep (1 of 6) 1892 1 IIGGKNSLRGGWPWQVSLRL.....PGVYTKVSAFVPWIKSVTKL

Scoring table: PAM 150 Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 30.953; Variance 131.070; scale 0.236

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

4 543 28.7 432 2 US-08-560-533 28.2 35.7 US-08-811-7 533 28.2 35.7 US-08-811-7 533 28.2 437 2 US-08-811-8 533 28.2 437 2 US-08-811-9 533 28.2 52.7 2 US-08-811-7 530 28.0 254 2 US-08-560-1530 28.0 254 2 US-08-560-1530 28.0 254 2 US-08-560-1530 28.0 254 2 US-08-560-1530 28.0 254 2 US-08-811-15-15-15-15-15-15-15-15-15-15-15-15-1	13211211111111111111111111111111111111	5433 5443 5443 5443 5443 5443 5443 5443		31111111111111111111111111111111111111	DB 1221221221221221222122212222222222222	8111111111 89088888888888888888888888888	Patta Sequence of the sequence	
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543 28.7 411 1 US-08-153- 543 28.7 430 4 51219569-2 543 28.7 431 4 51829569-1 543 28.7 431 4 51829569-1 543 28.7 432 2 US-08-811- 534 28.2 347 2 US-08-811- 533 28.2 355 2 US-08-811- 533 28.2 437 2 US-08-811- 533 28.2 437 2 US-08-811- 533 28.2 437 2 US-08-811- 530 28.0 254 2 US-08-811- 530 28.0 411 2 US-08-860- 527 27.9 354 2 US-08-811-		543 543	x x x	- - 9	2	-08-560 -08-087 -08-286	Sequenc	e 44, Applica e 1, Applicat e 18, Applicat
3 543 28.7 431 4 5188829-1 543 28.7 432 2 US-08-560-1 5534 28.2 347 2 US-08-811-1 6533 28.2 355 2 US-08-811-1 7533 28.2 437 2 US-08-811-1 9533 28.2 437 2 US-08-811-1 9533 28.2 437 2 US-08-811-1 9533 28.2 527 2 US-08-560-1 9530 28.0 254 2 US-08-560-1 9530 28.0 411 2 US-08-560-1 9537 27.9 354 2 US-08-811-1	21	543 543	œ œ	$\omega \vdash$	4	-08-153 19569-2	Sequence	18, Applica o. 5219569.
543 28.7 432 2 US-08-560-534 28.2 347 2 US-08-811-6533 28.2 355 2 US-08-811-7533 28.2 437 2 US-08-811-9533 28.2 437 2 US-08-811-9533 28.2 527 2 US-08-811-9530 28.0 254 2 US-08-560-1530 28.0 4254 2 US-08-560-1530 28.0 4254 2 US-08-560-1530 28.0 4254 2 US-08-560-1530 28.0 4254 2 US-08-811-1530 28.0 4254 2 US-08-811-153	13	543	œ	w	4	88829	Patent	No. 5188829
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US-08-217US-08-811US-08-811US-08-127US-08-217US-08-217US-08-217US-08-811US-08-811US-08-811US-08-811US-08-811US-08-811US-08-811US-08-811US-08-811US-08-811US-08-811US-08-811-PCT-US91-0 5344773-2 5244676-5 Sequence 16, Applicati Sequence 2, Applicatio patent No. 5344773. patent No. 5244676. Sequence 50, Applicati Sequence 38, Applicati Sequence 38, Applicati Patent No. 518559. patent No. 5200340. Sequence 45, A, Sequence 1, A, Sequence 1, A, Sequence 4, A, Sequence 6, A, Sequence 6, A, Sequence 55, Seque Sequence Sequence Patent

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ALIGNMENTS

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CKET NUMBER: ION INFORMATI 415-855-0555 5-845-4166 SEQ ID NO: 3 CTERISTICS:	CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTORNEY_AGENT INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749	6 B O S K O F	Sequence 3, Application US/08681151 Patent_NO	US-08-681-151-3 STANDARD; PRT; 638 AA xxxxxx • Sequence 3, Application US/08681151

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                                                                                                                                                                                                                                                                                                           Patent No. 5869637
GENERAL INFORMATION:
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                                                                               CURRENT APPLICATION DATA:
                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                               APPLICATION NUMBER: US
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     TITLE OF INVENTION: A NOVEL HUMAN KALLIKREIN NUMBER OF SEQUENCES: 4
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                    COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                           STREET: 3174 PO:
CITY: Palo Alto
STATE: CA
                       APPLICATION NUMBER:
                                                                                           SOFTWARE:
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                                                                                                                                                                                                  ADDRESSEE: INCYTE PHARMACEUTICALS, INC STREET: 3174 Porter Drive
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Braxton, Scott Michael
Goli, Surya
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                                                                                                                                                                                                                Patent No. 5648253
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 VLGINNLDHPSVFMQTRFVKTIILHPRYSRAVVDYDISIVEL--SEDISE--TGYVRPVC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      578 IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV 637
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Local Similarity 40.5%;
hes 98; Conservative
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                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                            APPLICANT: Wei, Cha-
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                CORRESPONDENCE ADDRESS
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CLONE: 307474
NCE 356 AA; 39995 MW;
                                                                                                COUNTRY:
                                                                                                                          CITY: Atlanta
                                                                                                                                        STREET:
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 APPLICATION NUMBER:
                                                                                                                                                    ADDRESSEE:
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                                                                                                            Georgia
                                                                                                                                       1100 Peachtree Street Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 amino acids
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                       PatentIn Release #1.0, Version
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US/07/942,1572
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Pred. No. 3.65e-42;
43; Mismatches 87;
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Best Local
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                                               Sequence 45, Application Patent No. 5976841 GENERAL INFORMATION:
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                                                                                                                                                                                                                                               355 TTKMLCAAD-POWK-TDSCOGDSGGPLVCSLOGRM-TLTGIVSWGRGCALKDKPGVYTRV 411
                                                                                                                                                                                                                                                                                     297 ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (404)815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide LOCATION: 1..19
OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                   APPLICANT:
APPLICANT:
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631673
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
                                                                                                                                                                                                   SHFLPWIRSHTK 423
                                                                                                                                                                                                                             TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV
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                                                                                                                                                                                        SAFVPWIKSVTK 821
                                                                                                                                                                                                                                                                   ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site LOCATION: 198..203 OTHER INFORMATION: /labe OTHER INFORMATION: /note
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REGISTRATION NUMBER: 3
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CLASSIFICATION:
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                                                                                      45, Application US/08560098A
                                                                                                                                                                                                                                                                                                                                                                                                                             R INFORMATION: /label= modified R INFORMATION: /note= "six amino acids deleted in mutant" 430 AA; 48366 MW; 975277 CN;
                                                                                                                                                                                                                                                                                                                                                                                       28.8%;
ilarity 36.9%;
Conservative
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AMINO ACID
                            WNENDT, Stephan
HEINZEL-WIELAND,
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/note= "
                                                                   US/08560098A
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Pred. No. 2.76e-41
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                                                                                                 Sequence 46, Application US/08560098A
                                        Sequence 46, Application US/08560098A Patent No. 5976841
                   Patent No. 5976841 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               231 TTKMLCAAD-PQWK-TDSCQGDSGGPLVCSLQGRM-TLTGIVSWGRGCALKDKPGVYTRV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      696 ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLFKRFCEE-RYKGR-F 749
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mes 93; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: US, APPLICATION NUMBER: US,
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TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: li
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                                                                                                                                                                                                                       STANDARD;
Stephan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 331 AA; 37442 MW;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: P 44
FILING DATE: 17-NOV-1994
ATTORNEY_AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Proteins having Fibrinolytic and TITLE OF INVENTION: Coagulation-inhibiting Properties NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                   SAFVPWIKSVTK 821
                                                                                                                                                            SHFLPWIRSHTK 299
                                                                                                                                                                                                                                                                                    RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP 695
                                                                                                                                                                                                                                                                                                            YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 172
                                                                                                                                                                                      TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV
                                                                                                                                                                                                            TTKMLCAAD-POWK-TDSCQGDSGGPLVCSLQGRM-TLTGIVSWGRGCALKDKPGVYTRV 287
                                                                                                                                                                                                                                                                                                                                    IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV 637
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           83, Application US/08720012
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ilarity 36.9%;
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30 (EPO)
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                                                                                    STANDARD;
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Pred. No. 4.32e-41;
60; Mismatches 85;
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Suite 700
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Local Similarity 36.9%;
hes 93; Conservative
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INFORMATION FOR SEQ ID NO: 83:
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: EVANS, JOSEPH D. REGISTRATION NUMBER: 26,269 REFERENCE/DOCKET NUMBER: 148 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)628-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/093,741
FILING DATE: 20-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 27-SEP-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                              SHFLPWIRSHTK
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                                                SAFVPWIKSVTK
                                                                                                TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV
                                                                                                               TTKMLCAAD-PQWK-TDSCQGDSGGPLVCSLQGRN-TLTGIVSWGRGCALKDKPGVYTRV
                                                                                                                                                ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRECEE-RYKGR-F
                                                                                                                                                                        ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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(202)628-8844
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Pred. No. 4.32e-41;
60; Mismatches 85
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                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P43 23
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202,628-8800
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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COMPUTER READABLE FORM:
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           SHFLPWIRSHTK 358
                                                    TTKMLCAAD-PQWK-TDSCQGDSGGPLVCSLQGRM-TLTGIVSWGRGCALKDKPGVVTRV 346
                                                                                         ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F 749
                                                                                                                                             RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP 695
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                                                                                                           ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV 289
                                       TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/093,741 FILING DATE: 20-JUL-1993 CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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93; Conservative
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HEINZEL-WIELAND, REGINA
SAUNDERS, DEREK J.
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Pred. No. 4.32e-41;
60; Mismatches 85;
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                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/560,098A
FILLING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILLING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                                                                                                                                                                            Local Similarity
es 93; Conse
                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acid
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                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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APPLICANT: STEFFENS, Gerd JOSE:
TITLE OF INVENTION: Coagulation-inhibiting Properties
"""" OF SEOUTNCES: 60
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MEDIUM TYPE: Floppy
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TTKMLCAAD - PQWK - TDSCQGDSGGPLVCSLQGRM - TLTGIVSWGRGCALKDKPGVYTRV
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                          ACLP-LWRERPOKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F
                                              ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV 290
                                                                        RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP 695
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                                                                                                                   Local Similarity 36.9%; es 93; Conservative
                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                           TYPE: all....
STRANDEDNESS: N/A
TOPOLOGY: N/A
TOPOLOGY: N/A
411 AA; 46367 MW; 892190 CN;
NO. 44.
                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,983
REFERENCE/FOCKET NUMBER: 04:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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APPLICANT: Gurewich, Victor
TITLE OF INVENTION: PRO-UROKINASE MUTANTS
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ACLP-LWRERPOKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                              TELLEFAX: (UL
TELEFAX: 200154
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                       ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV 335
                                           RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP
                                                           YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 277
                                                                               IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2 Model 502 or 55 OPERATING SYSTEM: MS-DOS (Version
                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: UFILING DATE: 07/02/93
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 225
CITY: Boston
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                                                                                                                                                                                           LENGTH:
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AL INFORMATION:
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225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                          WordPerfect (Version 5.1)
                                                                                                                          28.7%;
                                                                                                                                                                                                                                                                          J. Peter
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2 Model 50Z or 55SX
                                                                                                               Score 543; DB 1; Lenv. Pred. No. 4.32e-41; Pred. No. 4.32e-41;
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                                                                                                                                    Sequence 18, Application US/08286748B
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les 93; Conser
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INFORMATION FOR SEQ ID NO:
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LENGTH: 411
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Di
COMPUTER: IBM PS/2 M
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
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                                                                YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 277
RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: J. Peter Fasse REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: August 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                        411 AA; 46367 MW; 892190 CN;
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                                                                                                                                                                                                                                                                                                               Score 543; DB 1;
Pred. No. 4.32e-41;
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                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Swope, R Hain
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypept.
        TOPOLOGY: linear MOLECULE TYPE: prot
                                          SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acid
                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 665 2400
TELEPAX: (908) 771 6159
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                     TELEFAX: ();
TEV: 219484
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                                                                                                                         REGISTRATION NUMBER: 248
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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LE TYPE: protein
411 AA; 46367 MW; 892190 CN;
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Best Local Similarity 36.9%;
Matches 93; Conservative
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Best Local
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APPLICANT: BLABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5219569
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Local Similarity 36.9%;
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APPLICATION NUMBER: 725,468
FILING DATE: 22-APR-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PROTE NUMBER OF SEQUENCES: 6 CURRENT APPLICATION DATA:
                                                                          TTKMLCAAD-PQWK-TDSCQGDSGGPLVCSLQGRM-TLTGIVSWGRGCALKDKPGVYTRV 411
                                                                                                                                             ICLPSMYND-PQ-FGTSCEITGEGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F
SAFVPWIKSVIK
                           SHFLPWIRSHTK 423
                                                                                                                     ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F 749
                                                                                                                                                                                 RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP 695
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                                                          TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/766,858 FILING DATE: 16-AUG-1985
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 430
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821
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Pred. No. 4.32e-41;
60; Mismatches 85
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Pred. No. 4.32e-41;
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APPLICANT: KOBAYASHI, YO-ICH
TITLE OF INVENTION: RAPIDLY
NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 47, Application US/08560098A
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47, Application US/08560098A
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Local Similarity 36.9%;
les 93; Conservative
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COMPUTER READABLE FORM:
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TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
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                                                                  COUNTRY:
                                                                                                                                            ADDRESSEE: Evenson, McKeown, STREET: 1200 G Street, N.W.,
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FILING DATE: 18-AUG-1988
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HEINZEL-WIELAND, Regina
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60; Mismatches 85
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                                                                                                                                     Patent No.
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                      APPLICANT: HAYASHİ, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
ADDRESSEE: OBLON, S
                                                                                     APPLICANT:
                                                                                                APPLICANT:
                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                       SHFLPWIRSHTK 425
                                                                                                                                                                                                                                                                                                                                                                                             ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F 749
                                                                                                                                                                                                                                                                                                                                                                                                            ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                             RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 298
                                                                                                                                                                                                                                                                                               SAFVPWIKSVIK
                                                                                                                                                                                                                                                                                                                                               TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV 809
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TOPOLOGY: li
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COMPUTER: II
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                                                                                                                                     , Application US/08811949
5840533
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larity 36.9%;
Conservative
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 SPIVAK,
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Pred. No. 4.32e-41;
60; Mismatches 85
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 MCCLELLAND,
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 MAIER & NEUSTADT,
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Best Local Similarity 39.6%;
Matches 95; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 347 AA; 38594 MW; 612249 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                      108 PWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERF--PPHHLTVILGRTYR-VV 164
                                                            707 KTASNCYITGWG--DT-GRAYSRTLQQAAIPLLPKRFC-EERYKGR-FTGRMLCAGNLHE 761
                                                                                                                                                          224 PDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRS 283
                                                                                                                                                                                                                       165 PEEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPP-ADLQL 223
                                                                                                                                                                                           647 PEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQ 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIJM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                   Score 534; DB 2; Length 347; Pred. No. 3.26e-40; 52; Mismatches 76; Indels 17;
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h_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:17:02 2000; MasPar time 12.13 Seconds $603.296 \ Million cell updates/sec$

>US-09-147-947-6 (578-822) from US09147947A.pep (1 of 6)

Description: Perfect Score: Sequence: 1 IIGGKNSLRGGWPWQVSLRL......PGVYTKVSAFVPWIKSVTKL 245

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

1:swissprot

Database:

Statistics: Mean 44.933; Variance 67.314; scale 0.668

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PLASMINOGEN (EC 3.4.21	HEPATOCYTE GROWTH FACT	PLASMINOGEN (EC 3.4.21	UROKINASE-TYPE PLASMIN	OR (E		PLASMINOGEN (EC 3.4.21		TISSUE PLASMINOGEN ACT	PLASMINOGEN (EC 3.4.21		TISSUE PLASMINOGEN ACT	ACROSIN PRECURSOR (EC	_	PRECURSOR (TISSUE PLASMINOGEN ACT	ACROSIN PRECURSOR (EC	KALLIKREIN	PLASMA KALLIKREIN PREC	PLASMA KALLIKREIN PREC	COAGULATION FACTOR XI	NEUROTRYPSIN PRECURSOR	NEUROTRYPSIN PRECURSOR	Description
1.49e-99	8.09e-100	3.82e-101	1.13e-101	3.32e-102	5.30e-103	4.59e-104	1.16e-105	1.16e-105	4.67e-108	1.86e-110	1.01e-110	5.44e-111	3.97e-113	1.16e-113	5.33e-115	3.26e-118	1.40e-123	1.40e-123	3.41e-125	6.28e-132	0.00e+00	0.00e+00	Pred. No.

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24	504	σ	442	۰	UROK_PIG	UROKINASE-TYPE PLASMIN	1.49e-99
25	503	σ	812	Н	PLMN_BOVIN	PLASMINOGEN PRECURSOR	. 7
26	503	9	1019	Н	ENTK_HUMAN	ENTEROPEPTIDASE PRECUR	2.74e-99
27	501	26.5	431	سر	URTB_DESRO	SALIVARY PLASMINOGEN A	
28	499	26.4	394	ш	URTG_DESRO	SALIVARY PLASMINOGEN A	3.14e-98
29	499	26.4	477	₩	URT1_DESRO	SALIVARY PLASMINOGEN A	
30	499	26.4	477	<u>د م</u> ا	URT 2_DESRO	SALIVARY PLASMINOGEN A	
3 <u>1</u>	499	26.4	593	<u>سر</u>	FA12_BOVIN	COAGULATION FACTOR XII	
32	489	25.8	433	_	UROK_BOVIN	UROKINASE-TYPE PLASMIN	
33	487	25.7	810	μ.	PLMN_HUMAN	PLASMINOGEN PRECURSOR	4.69e-95
34	484	25.6	812	<u>ب</u>	PLMN_MOUSE	PLASMINOGEN PRECURSOR	
ω 5	481	25.4	434	Н	UROK_CHICK	UROKINASE-TYPE PLASMIN	1.80e-93
36	476	25.2	810	بــ	PLMN_MACMU	PLASMINOGEN PRECURSOR	3.74e-92
37	474	25.1	264	μ,	CTRL_HUMAN	CHYMOTRYPSIN-LIKE PROT	1.26e-91
38	472	24.9	433	μ	UROK_MOUSE	UROKINASE-TYPE PLASMIN	
39	472	24.9	603	ш	FA12_CAVPO	COAGULATION FACTOR XII	
40	467	24.7	1034	щ	ENTK_PIG	ENTEROPEPTIDASE PRECUR	
41	463	24.5	810	Н	PLMN_ERIEU	PLASMINOGEN PRECURSOR	9.86e-89
42	462	24.4	432	₩	UROK_RAT	UROKINASE-TYPE PLASMIN	1.81e-88
43	461	24.4	1035	Н	ENTK_BOVIN	ENTEROPEPTIDASE PRECUR	3.31e-88
44	460	24.3	4548	ப	APOA_HUMAN	APOLIPOPROTEIN(A) PREC	6.06e-88
45	456	24.1	615	μ	FA12_HUMAN	COAGULATION FACTOR XII	6.80e-87

ALIGNMENTS

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EMBL; AJ00 PROSITE; P PROSITE; P PROSITE; P PROSITE; P Hydrolase; SIGNAL CHAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN	This SWISS-PROT between the Swi the European Bio use by non-promodified and thi entities require or send an email	SEQUENCE FROM N.A. TISSUE=BRAIN; MEDLINE; 98201705. PROBA K., GSCHWEMU "Cloning and seque Biochim. Biophys!- FUNCTION: PLAY ACTION AND M LEARNING AND M -!- SUBCELLULAR LO	11 5-6730; 5-6730; 5-DEC-19 5-DEC-19 5-DEC-19 5-DEC-19 EUROTRYP RRSS12. omo sapi ukaryota ukaryota; 1]
AJ001531; C1 E; PS00134; E; PS00135; E; PS00420; ase; Serine 1 21 23 23 23 23 28 28 387	SWISS-PROT entry is en the Swiss Instiuropean Bioinformat by non-profit insied and this statem ies requires a licendan email to licendan email email to licendan email to licendan email to licendan email to licendan email e	UE-BRAIN, INE: 98201705. A K., GSCHWEND T.P., IN JAMEN T.	P: (i)
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GSCHWEND T.P., KRUEGER S
"Neurotrypsin, a novel m
nervous system.";
                                                                                                         SEQUENCE FROM N.A. MEDLINE; 98008848. YAMAMURA Y., YAMASH YAMAGUCHI N.;
                                                                                                                                                                                            (1)
EQUENCE FROM N.A.
PISSUE-BRAIN;
MEDLINE; 97401523.
                                                                                                                                                                                                                                                                                                                             NETR_MOUSE 008762;
                           Biochem. Biophys. Res. Commun. 239:386-392(1997).
-I- FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY!
ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS
LEARNING AND MEMORY OPERATIONS.
-I- TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL (
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15-DEC-1999 (Rel. 39, I
15-DEC-1999 (Rel. 39, I
NEUROTRYPSIN PRECURSOR
                                                                                                "Molecular cloning
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SUBCELLULAR LOCATION: SECRETED. SIMILARITY: BELONGS TO PEPTIDASE
                     AND AMYGDALA.
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dentzoa; Chordata; Craniata; Vertebrata;
dentia; Sciurognathi; Muridae; Murinae;
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larity 100.0%;
Conservative
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39, Last seguence update;
39, Last annotation update;
CURSOR (EC 3.4.21.-) (MOTOPSIN)
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2YMOGRAFION REGION.
REACTIVE BOND (POTENTIAL).
CHARGE RELAY SYSTEM.
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CHARGE RELAY SYSTEM.
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                                                AND THE PROTEOLYTIC
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Mus.
                                                                                    protease with cysteine-rich
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P03951;
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COAGULATION
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PFAM; PF00089; trypsin; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00420; SPERACT_RECEPTOR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y13192; CAA73646.1; -. EMBL; D89871; BAA23986.1; -. MGD; MGI:1100881; PRSS12.
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-!- SIMILARITY: CONTAINS
-!- SIMILARITY: CONTAINS
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(Rel. 0
(Rel. 3
FACTOR
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                                                               STANDARD;
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39,
XI
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89.8%;
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PRECURSOR (EC 3.4.21.27)
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3 SRCR DOMAINS.
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REACTIVE BOND (POTENTIAL).
CHARGE RELAY SYSTEM.
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POTENTIAL.
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RA MELJERS J.C., DAVIE E.W., CHUNG D.W.;

RA "Expression of human blood coagulation factor XI: characterization of the defect in factor XI type III deficiency.";

RI Blood 79:1435-1440(1992).

CC -!- FUNCTION: FACTOR XI TRIGGERS THE MIDDLE PHASE OF THE INTRINSIC CO. PATHMAY OF BLOOD COAGULATION BY ACTIVATING FACTOR IX.

CC -PATHMAY OF BLOOD COAGULATION BY ACTIVATING FACTOR IX.

CC -!- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF ARG-|-ALA AND ARG-|-VAL CC BONDS IN FACTOR IX TO FORM FACTOR IXA.

CC -!- SUBUNIT: HOMODIMER; LINKED BY A DISULFIDE BOND. AFTER ACTIVATION CC THE HEAVY AND LIGHT CHAINS ARE ALSO LINKED BY A DISULFIDE BOND.

CC -!- PIM: ACTIVATED BY FACTOR XIIA (OR XII), WHICH CLEAVES EACH POLYPEPTIDE AFTER ARG-387 INTO THE LIGHT CHAIN, WHICH CONTAINS THE ACTIVE SITE, AND THE HEAVY CHAIN, WHICH ASSOCIATES WITH HIGH MOLECULAR WEIGHT (HAW) KININGEEN.

-!- DISEASE: DEFECTS IN F11 ARE A CAUSE OF A BLOOD COAGULATION ABNORMALITY (ROSENTHAL SYNDROME) OCCURRING IN HIGH FREQUENCY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE, AND DISULTAND PARTIAL SEQUENCE, AND DISULTAND MEDLINE; 91152017, MCMULLEN B.A., FUJIKAWA K., DAVIE E.W.; "Location of the disulfide bonds in human coagulation factor XI: presence of tandem apple domains."; Biochemistry 30:2056-2060(1991).
  EMBL;
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                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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ASAKAI R., DAVIE E.W., CHUNG D.W.;
"Organization of the gene for human factor XI.";
piochemistry 26:7221-7228(1987).
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MEDLINE: 86243360.
FUJIRAWA K., CHUNG D.W., HENDF
"Amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT LEU-301.
MEDLINE; 92190478
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Eukaryota; Metazoa; (
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  M13142;
M20218;
M18296;
M18298;
M18299;
M18299;
M18300;
M18301;
M18301;
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  AAA51985 1;
AAA51985 1;
AAA51985 1;
AAA51985 1;
AAA51985 1;
AAA51985 1;
AAA51985 1;
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EMBL; M18304;
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EMBL; A27431; K
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134540; -
VYSGILNQSEIKED-TSFFGVQEIIIHDQYKMAESGYDIALLKLETTVN-YT--DSQR-P 498
                  IVGGTASVRGEWÞWQVTLH-TTSÞTQ-RHLCGGSIIGNQWILTAAHCF--YGVESÞKILR 443
            IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYG-NSTRSYA
                                            Similarity
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304; AAA51985.
217; AAA51985.
217; AAA51985.
31; KFHU1.
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Pred. No. 6.28e-132;
53; Mismatches 71:
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APPLE 1.
APPLE 2.
APPLE 3.
APPLE 4.
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C -> S (IN REF. 2).
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APPLE 2.
APPLE 3.
APPLE 4.
CATALYTIC.
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FACTOR
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XIA LIGHT CHAIN.
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A SEIDAH N.G., SAWYER N., HAMELIN J., MION P., BEAUBIEN G.,

A BEACHPAPA L., ROCHEMONT J., MEIKAY M., CHRETIEN M.;

A BRACHPAPA L., ROCHEMONT J., MEIKAY M., CHRETIEN M.;

Thouse plasma kallikrein: CDNA structure, enzyme characterization,

and comparison of protein and mRNA levels among species.";

TO A CELL Biol. 9:737-748(1990).

ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING

CONTROL AND ARECLEPROCAL REACTION, FACTOR XII AFTER ITS BINDING

CONTROL AND MAY ALSO PLAY A ROLE IN THE RENIN ANGIOTENSIN

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CONTROL A HEAVY CHAIN, WHICH ASSOCIATES WITH HMW KININOGEN. THESE

CONTROL ARE LINKED BY ONE OR MORE DISULFIDE BONDS.

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CONTROL AND ARE LINKED BY ONE OR MORE DISULFIDE BONDS.

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CONTROL BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYSIN FAMILY. BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYSIN FAMILY. BELONGS TO THE PLASMA KALLIKREIN SUBFAMILY.
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MGD; MGI:102889; KLK3.

PROSITE; PS00134; TRYPSIN_HIS;

PROSITE; PS00135; TRYPSIN_SER;

PROSITE; PS00495; APPLE; 4.
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PFAM; PF00089; trypsin;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PLASMA KALLIKREIN PRECURSOR (EC 3.4.21.34) (PLASMA PREKALLIKREIN)
                                                            DOMAIN
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ukaryota; Metazoa; (
utheria; Rodentia;
  CARBOHYD
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Blood coagulation; Inflammatory
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APPLE 2.
APPLE 3.
APPLE 4.
CATALYTIC.
PROBABLE.
PROBABLE.
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PLASMA KALLIKREIN LIGHT
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response; Liver;
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                                "Human plasma prekallikrein, a contains four tandem repeats."; Biochemistry 25:2410-2417(1986)
                                                            MEDLINE: 86243359...
CHUNG D.W., FUJIKAWA K., MCMULLEN B.A.,
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Rel. 02, Last sequence update)
Rel. 32, Last annotation update)
REIN PRECURSOR (EC 3.4.21.34) (PLASMA PREKALLIKREIN)
(FLETCHER FACTOR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      presence of four novel apple
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SUBUNIT: THE ZYMOGEN IS ACTIVATED BY FACTOR XIIA, WHICH CLEAVES
THE MOLECULE INTO A LIGHT CHAIN, WHICH CONTAINS THE ACTIVE SITE,
AND A HEAVY CHAIN, WHICH ASSOCIATES WITH HMW KININGEN. THESE
CHAINS ARE LINKED BY ONE OR MORE DISULFIDE BONDS.

DISEASE DEFECTS IN KLAS ARE THE CAUSE OF FLETCHER FACTOR
DEFICIENCY, A BLOOD COAGULATION DEFECT.

SIMILARITY: CONTAINS 4 APPLE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS T TRYPSIN FAMILY. BELONGS TO THE PLASMA KALLIKREIN SUBFAMILY.
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WEDLINE, 90091743.

KA SEIDAH N.G., LADENHEIM R., MBIKAY M., HAMELIN J., LUTFALLA G.,

KA ROUGEON F., LAZURE C., CHRETIEN M.;

"The DNA SITUCTURE OF TAT PLASMA KALLIKTEIN.";

LONA 8:563-574(1989).

"The CONA STRUCTURE OF TAT PLASMA KALLIKTEIN.";

LONA 8:563-574(1989).

"The CONA STRUCTURE CLEAVES LYS-ARG AND ARG-SER BONDS. IT

ACTIVATES, IN A RECIPROCAL REACTION, FACTOR XII AFTER ITS BINDING

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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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p14272;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PLASMA KALLIKREIN PRECURSOR (EC 3.4.21.34) (PLASMA PREKALLIKREIN)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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15-JUL-1998 (
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WAIER W:-M.,
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BABA T., KASHIWABARA S.
MEDLINE; 90253655.
CECHOVA D., TOEFFER-PETERSEN E., ZUCKER A., JONAKOVA V.;
TIS sperminogen a modified proacrosin? Isolation, purification, partial characterization of low-molecular-mass boar proacrosin.
                                                                                                                                                                                                                                                                                                                                  FOCK-NUZEL R., LOTTSPEICH F., HE "N-Terminal amino acid sequence other serine proteinases ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Boar acrosin is a two-chain n structure of the light chain; serine proteinases.";
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Eukaryota; Metazoa;
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15-JUL-1998 (Rel.
ACROSIN PRECURSOR
                                                                                                                                                   proteinase.
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Hoppe-Seyler's Z. Physiol. Chem. 361:1823-1828(1980).
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Eur. J. Biochem. 182:563-568(1989).
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J. Biol. Chem. 264:11920-11927(1989).
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Eutheria; Cetartiodactyla; Suina;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 84261484.
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"Activation and maturation mechanisms of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R., LOTTSPEICH F., HENSCHEN A., MULLER-ESTERL W.; sin is a two-chain molecule. Isolation and primary of the light chain; homology with the pro-part of
                                                                                                                                226:38-42(1987).
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e binding, novel
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                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER; PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete localization of the disulfide bridges and glycosylation sites in boar sperm acrosin.";
FEBS Lett. 275:139-142(1990).
-!- FUNCTION: ACROSIN IS THE MAJOR PROTEASE OF MAMMALIAN SPERMATOZOA.
IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT
IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
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ACROSOME.

CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.

SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
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IFGANEVVWGSNKPVKPPLQERF-VEEIIIHEKYVSGLEINDIALIKI-TPPVPCGPF---:: | : | :: | :: | : | |: |
                          IIGGKNSLRGGWPWQVSLRLKSSHGDGRL-LCGATLLSSCWVLTAAHCFKRYGNST--R-
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X14844; CAA32948.1;
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R -> Q (IN REF. 2).
IR -> VT (IN REF. 2).
P -> A (IN REF. 2).
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ACROSIN LIGHT
ACROSIN HEAVY
PRO-RICH.
INTERCHAIN.
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E RELAY SYSTEM
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                  Plasma;
SIGNAL
PROPEP
                                                                                                              PROSITE;
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                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatic. Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning a and tPA.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Int. Dairy J. 5:605-617(1995).

-!- FUNCTION: TPA CONVERTS PLASMINGEN TO PLASMIN BY HYDROLYZING A SINGLE R-V BOND IN PLASMINGEN. ACTIVE IN TISSUE REMODELING AND DESTRUCTION, PARTICULARLY IN FIBRINOLYSIS, AND IN CELL MIGRATION.
-!- CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN PLASMINGEN TO FORM PLASMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UROT_
                                                               PFAM; PF00089; trypsin;
                                                                                                                                                                                                  EMBL; X85800;
HSSP; P00750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE PLASMINGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q28198;
01-NOV-1997
                                                       Plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAVN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLAT.
                                                                                                                                                                                                                                                                                                                                                                                                         -!- MISCELLANEOUS: TPA ATTACHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634
                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-I DOMAIN
SIMILARITY: CONTAINS 2 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                               CHAIN OF FIBRIN.
                                                                                       PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRIRSTNVCAGYPRG-K-IDTCQGDSGGPLMCRDRAENTFVVVGITSWGVGCARAKRPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVLPACLPLWRERPQKTASNCYITGWG----DTGRAYSRTLQQAAIPLLPKRFCEE-R-YK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -IGPGCLPQFKAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLELCNSTRWYN
                  Kringle;
1
22
                                                                                                                                                                         PS00134; TRYPSIN_HIS; PS00135; TRYPSIN_SER;
                                                                                                               PS01253; FIBRONECTIN_1; 1.
PS00021; KRINGLE_1; 1.
PS50070; KRINGLE_2; 2.
                                                                                                                                                  PS00022; EGF_1;
PS01186; EGF_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BERGLUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Bovine).
Metazoa; Chordata; Craniata;
                                                     activation;
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                                                                                                                                                                                                              CAA59795.1; -
¿sin; 1.

_vation; Hydrolase; 5.

e; EGF like domain; c

21

By
                                                                                         EGF;
fn1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    818
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                  domain; Signal.
BY SIMILARITY
BY SIMILARITY
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the
                                                     Serine protease; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bovine plasminogen activators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     566 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pecora;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.4.21.68) (TPA)
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MBL outstation -
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Best Local
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                                                                                                                                                          ACRO_RAT
P29293;
01-DEC-1992
01-DEC-1992
01-NOV-1997
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CARBOHYD
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DOMAIN
       STRAIN-SPRAGUE-DAWLEY; TISSUE-TESTIS; MEDLINE; 92031708.
KLEMM U., FLAKE A., ENGEL W.;
                                                   SEQUENCE FROM N.A
                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Eutheria; Rodentia; Sciu
                                                                                                                                         01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
ACROSIN PRECURSOR (EC 3.4.21.10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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                                                                                                                                                                                                                                                                                                     RDNTR 565
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                                                                                                                                                                                                                                                                                                                                                               SGGDHTNLHDACQGDSGGPLVCMKDNHMTLV-GIISWGLGCGRKDVPGVYTKVTNYLDWI
                                                                                                                                                                                                                                                                                                                                                                                            KTA-SNCYITGWG--DTGRAY-SRTLQQAAIPLLPKRFC-EER-YKGRFTGRMLCAGNLH
                                                                                                                                                                                                                                                                                                                                                                                                                      LPDWTECELSGYGKHESSSPFFSERLKEAHVRLYPSSRCTSQHLFNRTVTNNMLCAGDTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWQAAIFVKNRRSPGERFLCGGILISSCWVLSAAHCFQERYPPHHLKVFLGRT--YR-LV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGEEEQTFEVEKYIIHKEFDDDTYDNDIALLHLKSDSLTCARESASVRTICLP--DASLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 29.7%;
Similarity 39.6%;
97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            566
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                                                                               Chordata; Craniata; Ver
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 562; DB 1; L
Pred. No. 5.33e-115;
53; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRINGLE 1.
KRINGLE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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                                                                                                                                                       update)
                                                                                                Vertebrata;
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                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 566;
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                                                                                Rattus
                                                                                             Mammalia;
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PIR; S18407; S18407.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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Biochim. Biophys. Acta 1090:270-272(1991).
-i- FUNCTION: ACROSIN IS THE MAJOR PROTEASE OF MAIT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAV IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
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                                                                                                                748
                                                                                                                                                                                                                             693
                                                                                                                                                                                                                                                                                                                                             634
                                                                                                                                                                                                                                                                                                                                                                                                                                                          578
  807
                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                     159
                                                                                                                                                                                                                                                                                                                                                                                                  103 VFGAHEIEYGRNKPVKEPQQERYVQKIVIHEKYNAVTEGNDIALLKV-TPPVTCGDF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFIDE BONDS
SIMILARITY: BELO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYPSIN FAMILY
                                                                                                                                                                                                                                                                   VGPGCLPHFKSGPPRIPHTCYVTGWGYIKDNAPRPSPVLMEARVDLIDLDLCNSTQWYNG
                                                                                                                                                   RVTSTNVCAGY-PEGK-IDTCQGDSGGPLMCRDTRRQPFVIVGITSWGVGCARAKRPGVY
  TKVSAFVPWIKS
                                                        TATWDYLDWIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preproacrosin-related cDNA.";
Biochim. Biophys. Acta 1219:15-218(1994).

-i- EUNCTION: ACROSIN IS THE MAJOR PROTEASE OF MAMMALIAN SPERMATOZOA
IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT
IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
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                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
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-IGPGCLPNSKAGPPKAAQTCYVAGWGYVKENAPRPSPTLMEARVDLINLELCNSTQWYN
                     RSYAVRVGDYHTLVPEEFE-EEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSS
                                         MVFGAQEIEYGTDKPVRPPLQERYVEKVVTHDQYNYMTEGNDIALLKI-TPPVPCGPF--
                                                               IIGGKNSLRGGWPWQVSLRLKSSHGDGRL-LCGATLLSSCWVLTAAHCF--K-R-YGNST
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Metazoa; Chordata; Craniata; Vertebrata;
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P23578;
01-NOV-1991
01-NOV-1991
15-JUL-1999
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J. Biochem. 108:785-791(1990).
                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                           KLEMM U.,
ENGEL W.;
                                                                                                  This
                                                                                                                                                                                                                                 chromosomal localization.
Genomics 11:828-834(1991)
                                                                                                                                                                                                                                                                                                                                     "Mouse preproacrosin: cDNA sequence, postmeiotic expression in spermatoge
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 92041732.
WATANABE K., BABA T., KASHIWABARA S
"Structure and organization of the
J. Biochem. 109:828-833(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Eutheria; Rodentia;
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ACROSOME.

CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREI

CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.

SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED
                                                                                                                                                                                                FUNCTION: ACROSIN IS THE MAJOR PROTEASE OF MAMMALIAN SPERMATOZOA IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE
                                                                                                                        TRYPSIN FAMILY.
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY
                                                                                    SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
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EMBL; S66245; EMBL; S64500;

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HSSP; P00763; 1DPO.
MGD; MGI:87884; ACR.
PROSITE; PS00134; TRYPSIN_SER; 1
PROSITE; PS00135; TRYPSIN_SER; 1
PROSITE; PS00135; TRYPSIN_SER; 1
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IGPCCLPHFKAGPPQIPHTCYVTGWGYIKEKAPRPSPVLMEARVDLIDLDLCNSTQWYNG
                                                                                                                                       IVSGQSAQLGAWPWMVSLQIFTSHNSRRYHACGGSLLNSHWVLTAAHCFDNKKKVYDWRL 102
                                                                                  VFGAQEIEYGRNKPVKEPQQERYVQKIVIHEKYNVVTEGNDIALLKI-TPPVTCGNF---
                                                   SYAVRVGDYHTLVP-EEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSH
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CAA36704.1;
AAA40124.1;
AAA37163.1;
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Pred. No. 5.44e-111
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VV -> AG (IN CAA36704 AND AAA40124).

T -> A (IN CAA36704 AND AAA40124).

D -> F (IN CAA36704 AND AAA40124).

F -> T (IN CAA36704 AND AAA40124).

QL -> HV (IN CAA36704 AND AAA40124).

QL -> HV (IN CAA36704 AND AAA40124).
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QP -> PA (IN CAA36704 AND AAA40124).

L -> F (IN CAA36704 AND AAA40124).

H -> Y (IN CAA36704 AND AAA40124).

SQYSGPRNYHYRFSTFEPLSNKDSEPFLHS -> PS.

LPLPLLHY (IN CAA36704, AAA40124 AND.)
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EK -> RE (IN CAA36704 AND AAA40124).

VDS -> ARO (IN CAA36704 AND AAA40124).

FVVVGITSWGVGCA -> LCGRGDHELGGRLC (IN
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P19637;
01-FEB-1991
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                                                                                                                                                                                                                                                                                                                                            FENG P., OHLSSON.M., NY T.;

"The structure of the TATA-less rat tissue-type plasminogen activator gene. Species-specific sequence divergences in the promoter predict differences in regulation of gene expression.";

J. Biol. Chem. 265:2022-2027(1990).

-i- FUNCTION: TTA. CONVERTS PLASMINOGEN TO PLASMIN BY HYDROLYZING AND SINGLE R-V BOND IN PLASMINOGEN. ACTIVE IN TISSUE REMODELING AND DESTRUCTION, PARTICULARLY IN FIBRINOLYSIS, AND IN CELL MIGRATION.

-i- CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-I-VAL BOND IN PLASMINOGEN TO FORM PLASMIN.

-i- MISCELLANEOUS: TPA ATTACHES TO THE KRINGLE STRUCTURE OF THE A
                                  EMBL;
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                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-I DOMAIN.
-!- SIMILARITY: CONTAINS 2 KRINGLE REGIONS.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO TRYPSIN FAMILY.
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Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Rodentia; Sciuroghathi; Muridae;
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01-NOV-1997 (Rel. 35, Last annotation update)
TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68) (TPA)
(T-PLASMINOGEN ACTIVATOR).
                                                                                                                                                                           or send
                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
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PROSITE: PS00186; EGF_2: 1.

PROSITE: PS00185; FIRSUBETIN_1: 1.

PROSITE: PS00021; KRINGLE_1: 2.

PROSITE: PS50070; KRINGLE_2: 2.

PROSITE: PS50070; KRINGLE_2: 2.

PFAM; PF000081; EGF; 1.

PFAM; PF000081; kringle: 2.

PFAM; PF00089; kringle: 2.

PFAM; PF00089; kringle: 2.

PFAM; PF00089; kringle: 1.

PFAM; PF00089; Kringle: 2.

PFAM; PF00089; Kringle: EGF-1ike domain; Signal.
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A31597; A31597.
A35029; A35029.
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                      -EHKRV-DSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKS
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STEFFENS G.J., HEYNEKER H
"Cloning and expression o.
coli.";
 MEDLINE; 96000858.
SPRAGGON G., PHILLI
DOBSON C.M., STUARI
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P00749;
21-JUL-1986
20-MAR-1987
15-DEC-1999
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"The complete amino acid
from human urine.";
hoppe-Seyler's Z. Physiol
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UROKINASE-TYPE PLASMINOGEN ACTIVATOR PRECUR
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chains.";
                                                                                                                                                                                                                                                                                                            MEDLINE; 8300
SCHALLER J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 83055
GUNZLER W.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RICCIO A., GRIMALDI G., VERDE P., SEBASTIO "The human urokinase-plasminogen activator Nucleic Acids Res. 13:2759-2771(1985).
                                                                                                                                                        MEDLINE; 83055099.
STEFFENS G.J., GUN
                                                                                                                                                                                                                                                                                                                                                                 Hoppe-Seyler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     poly(A)+ RNA.",
Proc. Natl. Aca
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NISHIDA M., SUYAMA
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Eukaryota; Metazoa;
Eutheria; Primates;
                                                                     X-RAY CRYSTALLOGRAPHY (2.5
                                                                                                                                                                                          SEQUENCE OF 158-410.
                                                                                                                                                                                                                                                                                               STUDER R.O.;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 156-176 AND
                                                                                                                                                                                                                                                                                                                                                                                               "The primary structure of high molecular mass urokinase urine. The complete amino acid sequence of the A chain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERDE P., STOPPELLI
"Identification and
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J., NICK
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83055084.
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PHILLIPS C., NOWAK U.K., PO
STUART D.I., JONES E.Y.;
structure of the catalytic
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etazoa; Chordata; Craniata;
imates; Catarrhini; Hominid;
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                                                                                                                                                                                                                                                          preliminary
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n. 363:1155-1165(1982).
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                                                                                                       363:1043-1058(1982)
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VARIANT LEU-141.

WEDLINE; 96186279.

WOSHIMOTO M., USHIYAMA Y., SAKAI M., SAWASAKI Y., HANADA K.;

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"Mutational analysis of the genes encoding urok activator (uPA) and its inhibitor PAI-1 in advaelectrophoresis 18:686-689(1997).

-i- FUNCTION: POTENT PLASMINOGEN ACTIVATOR AND THERAPY OF THROMBOLYTIC DISORDERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 97337920.
TURKMEN B., SCHMITT M.,
CREUTZBURG S., GRAEFF F
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                                                                                                                                                                                                                                                                                                                                                                                                                               <del>.</del>
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structure.";
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Structure 3:681-691(1995).
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MEDLINE; 97337920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol.
                                                                                                                                                                                                               CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN PLASMINOGEN TO FORM PLASMIN.

SUBUNIT: FOUND IN HIGH AND LOW MOLECULAR MASS FORMS. EACH CONS OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM CONTAINS LONG CHAIN A. CLEAVAGE OCCURS AFFER RESIDUE 155 IN THE LOW MOLECULAR MASS FORM TO YIELD A SHORT A1 CHAIN.

PHARMACEUTICAL: AVAILABLE UNDER THE NAME ABBOKINASE (ABBOTT).

IN PULMONARY EMBOLISM (PE) TO INTIATES FIBRINOLYSIS.

SIMILARITY: CONTAINS 1 KRINGLE REGION.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                        TRYPSIN FAMILY
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78:973-973(1997).
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advanced ovarian cancer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X02419; CAA26268.1;
EMBL; M15476; AAA61253.1;
EMBL; D00244; BAA00175.1;
EMBL; K03226; AAC97138.1;
EMBL; K03226; AAC97138.1;
EMBL; K02286; AAA61252.1;
EMBL; A21571; CAA01359.1;
EMBL; A18397; CAA01390.1;
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PIR; A32974;
PDB; 1KDU; 31
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DOMAIN
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PROSITE;
PROSITE;
PROSITE;
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                         SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                             Plasminogen activation; Hydrolase; Eringle; EGF-like domain; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00051; kringle; PFAM; PF00089; trypsin;
                                                                                                                                                                                    ACT_SITE
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                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                         Pharmaceutical
638
               238
                              578
                                                                                          remainder
                                             179
RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP
                                            IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLMSPCWVISATHCFIDYPKKE-DYIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1LMW; 29-JAN-96
1URK; 08-MAY-95
              YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT
                            n 28.8%;
Similarity 36.9%;
93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PS00134; TRYPSIN_HIS; 1.
PS00135; TRYPSIN_SER; 1.
PS01186; EGF_2; FALSE_NEG
PS50070; KRINGLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00021;
PS00022;
PS00134;
                                                                                          of
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86
97
106
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                                                                                          annotations
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107
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431
177
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                                                           Score 545; DB 1; L
Pred. No. 1.86e-110;
60; Mismatches 85;
                                                                                                                                                                                                                                               CLEAVAGE (CATALYTIC BY SIMILAF BY SIMILAF BY SIMILAF
                                                                                                                                                                                                                                                                                                                                         UROKINASE-TYPE I UROKINASE-TYPE I LONG A CHAIN.
                                                                                                                                                                            CHARGE
CHARGE
CHARGE
                                                                                                                               /FTId=VAR_006722.
M -> I (IN REF. 3).
                                                                                                                                                     P -> L (RARE POLYMORPHISM;
DECREASE IN THE AFFINITY FO
                                                                                                                                                                                                                                                                                                                    UROKINASE-TYPE
                                                                                                                                              BINDING
                                                                                                                                                                                                                                                                                            KRINGLE
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SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                            CHAIN
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Signal; Polymorphism;
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                                                                                                                                                                            SYSTEM.
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PLASMI NOGEN
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                                                            Indels
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ACTIVATOR
                                                                                                                                                      DR FIBRIN-
                                                                                                                                                                                                                                                                                                                    ACTIVATOR
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                                                            Gaps
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    DOMAIN
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DOMAIN
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SCHALLER J., MARTI T., ROESSELET S.J., KAEMPFER U., RICKLI E.E.;

"Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the carbohydrate attachment sites with the human and bovine species.";
                                                                                                                                                                                               PFAM; PF00051; kringle; 5. PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 450-790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibrinolysis 1:91-102(1987).
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                                                                                                                                                                                                                                                                                                                                       TRYPSIN FAMILY. BELONGS; A25834; A25834.; S03733; S03733.
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                                                                                                                                                                                                                                         PS50070; KRINGLE_2;
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                                                                                                                                                                               Serine protease;
      561
561
84
166
256
358
461
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KRINGLE_2; 5.
      162
243
333
435
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HEAVY CHAIN I
LIGHT CHAIN I
CATALITIC.
KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
KRINGLE 5.
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Best Local
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.
(T-PLASMINOGEN ACTIVATOR).
                                                                                                                                                                                                                                                                                                                                                        RICKLES R.J., DARROW A.L., STRICKLAND S. "Molecular cloning of complementary DNA activator manA and its expression during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLAT
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 88087303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UROT_MOUSE P11214;
                                                                                                                                                                                                                                                                                                                                             differentiation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               815 WIKSVTK
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                                                                                                                                                                                                                                                 Biol. Chem. 263:1563-1569(1988).
FUNCTION: TPA CONVERTS PLASMINOGEN TO PLASMIN BY HYDROLYZING FUNCTION: TPA CONVERTS PLASMINOGEN TO PLASMIN BY HYDROLYZING SINGLE R.Y. BOND IN PLASMINOGEN. ACTIVE IN TISSUE REMODELING A DESTRUCTION, PARTICULARLY IN FIBRINOLYSIS, AND IN CELL MIGRAT CATALYTIC ACTIVITY: SPECIFIC CLEAVAGE OF ARG-|-VAL BOND IN PLASMINOGEN TO FORM PLASMIN.
                                                                                                                                                        SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE-I DOMAIN
SIMILARITY: CONTAINS 2 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO
                                                                                                                                                                                                                                      MISCELLANEOUS: TPA ATTACHES TO THE KRINGLE STRUCTURE OF
                                                                                                                                               TRYPSIN FAMILY.
                                                                                                                                                                                                                       CHAIN OF FIBRIN.
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Pred. No. 4.67e-108;
57; Mismatches 70;
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PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00122; EGF_1; 1.

PROSITE; PS00122; EGF_1; 1.

PROSITE; PS01253; FIBRONECTIN_1; 1.

PROSITE; PS01253; FIBRONECTIN_1; 1.

PROSITE; PS00021; KRINGLE_1; 2.

PROSITE; PS00070; KRINGLE_2; 2.

PROSITE; PS00070; KRINGLE_2; 2.

PFAM; PF00008; EGF; 1.

PFAM; PF00009; Kringle; 2.

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PROSITE; PS0013:
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819 VTK 821
                                                                                                                                                                                                                                                                                                                                                                           321 PWQAAIFVKNKRSPGERFLCGGVLISSCWVLSAAHCFLERFP-PNH-LKVVLGRTYR-VV 377 | | | | : : | : : | | : | | : | | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : : | : : : : : | : : : : : | : : : | : : : :
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                                                           556 NMK 558
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                                                                                                                                                                                                  707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y Match 27.9%;
Local Similarity 38.3%;
nes 93; Conservative
                                                                                                                           GGNQDLHDACQGDSGGPLVCMINKQM-TLTGIISWGLGCGQKDVPGVYTKVTNYLDWIHD 555
                                                                                                                                                                                         PGEEEQTFEIEKYIVHEEFDDDTYDNDIALLQLRSQSKQCAQESSSVGTACLPD-PNLQL 436
                                                                                                 --HKRV-DSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKS
                                                                                                                                                                                                                                                                                     PEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQ 706
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 527; DB 1; Le
Pred. No. 1.16e-105;
56; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE PLASMINOGEN ACTIVATOR A CHAIN (HEAVY).
TISSUE PLASMINOGEN ACTIVATOR B CHAIN (LIGHT, SERINE PROTEASE).
FIBRONECTIN TYPE-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plase; Serine protease; Glycoprotein;
nain; Signal.
PROBABLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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Search completed: Mon Mar 13 10:17:16 2000 Job time : 14 secs.

Tabular output not generated. h_pp Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Mon Mar 13 10:17:33 2000; MasPar time 29.51 Seconds 575.711 Million cell updates/sec

(MT)

Description: Perfect Score: Title:

Sequence: >US-09-147-947-6 (578-822) from US09147947A.pep (1 of 6) 1892 1 IIGGKNSLRGGWPWQVSLRL......PGVYTKVSAFVPWIKSVTKL 245

Scoring table: РАМ 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

T:Sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 43.807; Variance 67.987; scale 0.644

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

At Mo. of Es avoidable

21	485	Çī	810	4	151	46
22	478	25.3	277	σ	096899	
23	474		613	ω	Q03711	
24	471	٠.	454	σ	046506	
25	470	24.8	265	رى رى	Q17800	
26	467	4.	271	4	043342	
27	464	4.	603	11	Q61129	
28	464	24.5	616	0	097507	
29	462	4.	247	υ	Q17039	
30	462	4.	604	11	Q9WUW3	
31	449	ω ·	385	ഗ	Q25101	
32	444	ω.	267	4	Q15664	
33	442	ω.	.246	11	088301	
34	439	w •	266	13	Q92077	
35	439	ω.	275	4	Q15661	
36	435	ω	251	11	054854	
37	433	2	597	11	035727	
38	432		1004	13	P79953	
39	428	2	242	13	Q9W7Q7	
40	427	.2	482	11	Q63207	
41	423	2	358	υı	045029	
42	422	2	238	13	Q9W7Q6	
43	422	ν.	266		Q9W7Q0	
44	422	22.3	387	υī	09XY57	
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ALIGNMENTS

Qy	Db	Qy	B	Qy	Db	Qy	Дb	Qy	Ъ	Que Bes Ma	SQ	DR	DR	RL	77 2	Z E	RX	RP	R (88	88	DE	DT	Ţ	Į A	i i	RESULT
813 VPWI 816	561 VDWI 564	753 MLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAF 812	Y-REGGK-DACKGDSGGPLSC-KHNEVWHLVGITSWGEGCAQREF	696 ACLPLWRERPQKTASNCYITGWG-DTGRA-YSRTLQQAAIPLLPKRFCEERYKG-RFTGR 752	CWVTGWGYRKLRDKIQNTLQKAKIPLVTNE	DRSD	390 VYSGILNQSEIKED-TSFFGVQEIIIHDQYKMAESGYDIALLKLETTVN-YTDSQR-P 444	578 IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYG-NSTRSYA 636	-TTSPTQ-R	Query Match 33.0%; Score 625; DB 4; Length 571; Best Local Similarity 41.8%; Pred. No. 1.12e-127; Matches 102; Conservative 53; Mismatches 71; Indels 18; Gaps 16;	SEQUENCE 571 AA; 63840 MW; C25DB1A9 CRC32;	95; APPLE; 3.		787-13793(1998)	product of the plasma factor XI gene.":	SESHSMMA I., BAGASKA O	98256306.	SEQUENCE FROM N.A.		Eutheria: Primates: Catarrhini: Hominidae: Homo.			(TrEMBLrel. 12, Last	01-NOV-1999 (Translite1, 12, Last sequence update)	(Trevers) 10	Q9Y495 PRELIMINARY; PRT; 571 AA.	

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                                                                                                                                                            "The cortical granule serine protease CGSP1 of the sea urchin, Strongylocentrotus purpuratus, is autocatalytic and has an LDL receptor-like domain.";
Dev. Biol. 0:0-0(1999).
         PROSITE; PS01209; LDLRA_1; 3.
Signal; Protease; Glycoprotein.
SIGNAL 29 PC
CHAIN 30 581 CC
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. HALEY S.A., WESSEL G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CORTICAL GRANULE SERINE PROTEASE 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB030007; BAA82522.1; --
PROSITE; PS01209; LDLRA_1; 3.
Signal; Protease; Glycoprotein.
SIGNAL 1 28 PC
SEQUENCE 868 AA; 97660 MW;
                                                                                                                             Dev. Biol. 0:0-0(1999).
EMBL; AF149789; AAD37426.1;
                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TUNICATE RETINOIC ACID-INDUCIBLE MODULAR PROTEASE PRECURSOR.
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LPLWRERPQ-KTASNCYITGWG-D--TG-RAYSRTLQQAAIPLLPKREC--EERYKGRFT
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100; Conser
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larity 39.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 620; DB 5; Le
Pred. No. 2.25e-126;
56; Mismatches 77;
POTENTIAL.
CORTICAL GRANULE SERINE PROTEASE
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.3%;
Best Local Similarity 39.1%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Q29015;
01-NOV-1996
01-NOV-1996
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. Hoppe-Seyler 377:261-265(1996)
EMBL; X58549; CAA41440.1; -
PFAM; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
CHAIN 17 415 ACROSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metaztiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conservation among mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADHAM I.M., KREMLING H., NIETER S SCHROETER U., ENGEL W.; "The structures of the bovine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREPROACROSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
273
                                         747
                                                                                                                                      692
                                                                                                                                                                                                                                   634
                                                                                                                                                                                                                                                                                                                                578
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                                                                                        215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 IVGGQPATAGDWPWQAQLFYRT-RGSWQLVCGGTLIDPQVVLTAAHCFMGPMMATSRWQV
                                                                                                                                                                                                                                                                                                                                                      GRIRSTNYCAGYPRG-K-IDTCQGDSGGPLMCRDRAENTFYVYGITSWGYGCARAKRPGV 272
YTSTWPYLNWIAS
                                            GRFTGRMLCAGNLHEHKRVDSCQGDSGGPLMC-ERPGESWVYYGVTSWGYGCGVKDSPGV
                                                                                                                                      HVLPACLPLWRERPQKTASNCYITGWG---DTGRAYSRTLQQAAIPLLPKRFCEE-R-YK
                                                                                                                                                                                  -IGPGCLPQFKAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLELCNSTRWYN 214
                                                                                                                                                                                                                                 SYAVR-VG-DYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSS
                                                                                                                                                                                                                                                                             IFGANEVVWGSNKPVKPPLQERF-VEEIIIHEKYVSGLEINDIALIKI-TPPVPCGPF-- 155
                                                                                                                                                                                                                                                                                                                              IIGGKNSLRGGWPWQVSLRLKSSHGDGRL-LCGATLLSSCWVLTAAHCFKRYGNST--R- 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVPWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMLCAGNLHEHKRVDSCQGDSGGPLMCERPGE$WVVYGVTSWGYGCGVKDSPGVYTKVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TMLCAGHL-EGG-IDACQGDSGGPLSCLGPDDHWYVVGVTSWGHGCAIANKPGVYTKVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACLPLWRERPOKTASNCYITGWGDTGRA-YSR-TLQQAAIPLLPKRFCE-ER-YKGRFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACLD--EGMPLNDRTECYISGWGVTEMGGNGPDVLHEARMPLIPRRICNYKKSYNGKIEK 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVGDYHT-LVPEEFEEEIGVQQIVIHREYRPDRS-DYDIALVRLQGPEEQCARFSSHVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLGKHSVDFVPEAGSQHRLVREIFVHKKFGEHGGVGCDIALLILDEPVPQ-E--TGQINW 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΑA;
285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64438
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01,
12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              • 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WW;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 574; DB 6; I
Pred. No. 2.07e-114;
56; Mismatches 79:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 588; DB 5;
Pred. No. 4.81e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80A12323 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes
                                                                                                                                                                                                                                                                                                                                                                                                                           19;
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RESULT 5
ID 79343
AC P79343;
DT 01-MAY-1
DT 01-MAY-1
DT 01-NOV-1
DE ACROSIN:
OS Bos taur
OC Eutheria
OC Eutheria
B
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                        Q9Y5Q5;
Q9Y5Q5;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                            conservation among mammals.";
Biol. Chem. Hoppe-Seyler 377:261-265(1996).
EMBL; X68212; CAA48294.1; -.
HSSP; P00763; 1DPO.
PFAM; PF00009; LTYPSin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SEQUENCE 377 AA; 41722 MW; E646321D CRC.
                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                    CORIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=LIVER;
KEIME S.;
                                   Eutheria;
                                                                              01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADHAM I.M., KREMLING SCHROETER U., ENGEL W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER;
MEDLINE; 96348713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997
01-NOV-1999
  TISSUE=HEART;
            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The structures of the bovine and porcine proacrosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                       IFGAKEVEWGSNKPVKPPLQERY-VEKIIIHEKYSASSEANDIALIKITPPVI-CGHF-- 118
                                                                                                                                                                                                                                                                                                                                                                  IIGGQDAAHGSWPWMVSLQIFTYHNNRRYHVCWGLLLNAHWLLTAAHCFRIKKKVTDWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTKVSAFVPWIKS
                                                                                                                                                                                                                               GRIRSTNVCAGY-PEGK-IDTCQGDSGGPLMCKDSVENSYVVVGITSWGVGCSRAKRPGV
                                                                                                                                                                                                                                                            -IGPGCLPQFRAGPPRVPQTCWVAGWGFLRENARRTSPVLQEAHVDLIDLDLCNSTRWYN 177
                                                                                                                                                                                                                                                                                                          SYAVR-VG-DYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSS 691
                                                                                                                                                                                                                                                                                                                                                     IIGGKNSLRGGWPWQVSLRLKSSHGDGRL-LCGATLLSSCWVLTAAHCFK-RYGNST-R-
                                                                                                                                                                       YTKVSAFVPWIKS
                                                                                                                                                                                            YTSTWSYLNWIAS 248
                                                                                                                                                                                                                  GRFTGRMLCAGNLHEHKRVDSCQGDSGGPLMC-ERPGESWVVYGVTSWGYGCGVKDSPGV
                                   Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cetartiodactyla;
                                                                            ) (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Bovine)
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                                                                                                                                                                                                                                                                                                                                                                                                  29.5%;
llarity 37.9%;
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                                   Catarrhini;
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Last sequence update)
Last annotation updat
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Pred. No. 2.88e-110;
56; Mismatches 82;
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Last annotation update)
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                                           Craniata; Vertebrata;
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                                   Hominidae;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordaţa; Craniata; Vertebrata;
Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GERTON G.L., HOFF H.B., BABA T.; Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=HARTLEY; TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 99262646.

YAN W., SHENG N., SETO M., MORSER J.,
"COrin, a mosaic transmembrane serine
from human heart.";

J. Biol. Chem. 274:14926-14935(1999).
EMBL; AF133845; AAD31850 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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Local Similarity 40.5%;
hes 98; Conservation
                                                                                                                                                                                                                                         41 IIGGQTAQPGAWPWMVSLQIFMAHNNRRYHACGGILLNSHWVLTAAHCFDSKKKVYDWRL 100
-IGPGCLPTERAGPPKIPQTCYVAGWGYIREKAPRPSPVLLEARVELIDLDLCNSTQWYN : |: || | | : | : |: ::|: ::|:
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                                                                                  SYAVRVGDY -- HTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSS 691
                                                                                                                                   VFGAEEIEYGNNKPVRAPLQERY-VEKIVIHEKYNIVNEGNDIALLKITPPVS-CGPF-- 156
                                                                                                                                                                                       IIGGKNSLRGGWPWQVSLRLKSSHGDGRL-LCGATLLSSCWVLTAAHCF--KRYGNSTR- 633
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Similarity 39.1%;
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                                                                                                                                                                                                                                                                                                                      Score 545; DB 11;
Pred. No. 6.61e-107;
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Pred. No. 3.12e-109;
                                                                                                                                                                                                                                                                                                                                                                                                     PROACROSIN
52A9F199
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Q14520
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                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00051; kringle; PFAM; PF00089; trypsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                     YOSHIMOTO M., USHIYAMA Y., SAKAI M., TAMAKI S., F
SAWASAKI Y., HANADA K.;
"Characterization of single chain urokinase-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 96186279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 36:183-188(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lomo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                      ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRECEE-RYKGR-F
                                                                                                                                                                                  RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP
                                                                                                                                                                                               YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 277
                                                                                                                                                                                                                               IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV
                                                                                                                                                                                                                                                   IIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKE-DYIV 217
                                             SAFVPWIKSVTK
                                                                  SHFLPWIRSHTK
                                                                                          TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV
                                                                                                                                                           ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV
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                                                                                                                                                                                                                                                                           h 28.7%;
Similarity 36.9%;
93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86056954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIRAMATSU R.,
                                                                                                                                                                                                                                                                                                                    1
121
411 AA;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                   404
                                             821
                                                                                                                                                                                                                                                                                                                     121 L
46384 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KANEDA T.,
                                                                                                                                                                                                                                                                         Score 543;
Pred. No. 2
60; Mismat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Last sequence update)
, Last annotation update)
ACTIVATER (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding
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                                                                                                                                                                                                                                                                                                                                 ۲
PRT;
                                                                                                                                                                                                                                                                                                                     254CBB0E
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                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAYASUKE N.,
                                                                                                                                                                                                                                                                           3; DB 4; Le
. 2.17e-106;
matches 85;
560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                     REF. 1).
CRC32;
ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                          kringle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preprourokinase.";
                                                                                                                                                                                                                                                                                                Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARIMURA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HARA
                                                                                                                                                                                                                                                                                                                                                                                                                                    plasminogen activator
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                                                                                                                                                                                                                                                                                                                                                                                                                          structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAKAHASHI K.,
                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                           Gaps
                                                                                                               392
                                                                                                                                                                                  695
                                                                                                                                                                                                                               637
                                                                                         809
                                                                                                                                      749
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RESULT 10 09 AC 00                                                                                                                                                                                                                                                                                                                                   ESULT 10
D 92319;
C 92319;
C 092319;
C 092319;
T 01-MAY-1999 (TrEMBLrel. 10, Created)
JT 01-MAY-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DT 01-NOV-1999 (TREMBLREL. 12, Last annotation update)
DE LOW DENSITY LIPOPROTEIN RECEPTOR RELATED PROTEIN 4.
OS Mus musculus (Mouse)
OS Mus musculus (Mouse)
Chordata; Craniata; Vertebrata; Musiarvota; Metazoa; Chordata; Craniata; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC DESCRIPTION OF THE PROPERTY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S83182; AA
HSSP; P00763; 1D
PFAM; PF00008; F
                                                                                                     TOMITA Y., KIM D.-H., MAGOORI K., FUJINO T., YAMAMOTO T.T.
"A novel low-density lipoprotein receptor-related protein
membrane protein-like structure is abundant in heart.";
J. Biochem. 124:784-789(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00051; kringle; 1.
PFAM; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE
PRINTS; PR00702; CHYMOTRYPSIN.
SEQUENCE 560 AA; 62671 MW;
EMBL; AB013874; BAA34371.1; HSSP; P00763; 1DPO. PROSITE; PS01209; LDLRA_1; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q14520; 000663;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 98429596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Purification and characterization of a novel hyaluronan-bindi
protein (PHBP) from human plasma: it has three EGF, a kringle
serine protease domain, similar to hepatocyte growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
[1]
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CHOI-MIURA N.H., TOBE T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. KITAMURA N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D49742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGF ACTIVATOR LIKE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKSVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DTCQGDSGGPLTCEKDG-TYYYYGIVSWGLECG-K-RPGYYTQVTKFLNWIKATIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASNCYITGWG--DTGRAYSRTLQQAAIPLLPKRFCEER--YKGRFTGRMLCAGNLHEHKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EE-IGVQQIVIHREY--RPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP---DGSFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAVRVGDYHTLVPEEFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
99; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96425001
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MAR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119:1157-1165(1996).
2; BAA08576.1; -.
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8; EGF; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Α
LDLRA_1; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%;
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45; }
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Last annotation updat
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No. 7.12e-106;
73;
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- +hree EGF, a kringle and
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                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
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SQ

Glycoprotein. SEQUENCE 1113 AA;

122984 MW;

ABADC31E CRC32;

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815

WIKSVTK 821

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RESULT 11

O18783;
AC O18783;
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1998 (TrEMBLrel. 12
DT 01-NOV-1999 (TrEMBLrel. 12
DE PLASMINOGEN.
OS Macropus eugenii (Tammar v
OC Eukaryota; Metazoa; Chorde
OC Metatheria; Diprotodontia.
RN [1]
RP EMBLRENIVER;
RA LAWN R.M., SCHWARTZ K., P)
RI Submitted (JUL-1997) to tl
DR EMBL; AF012297; AAB65760.
DR HSSP; P00747; SHPG.
DR PEAM; PF00051; Kringle; 5
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Best Local
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PFAM; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYESIN.
SEQUENCE 806 AA; 90980 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAWN R.M., SCHWARTZ K., PATTHY L.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF012297; ABA65760.1; -.
HSSP: P00747; 5HPG.
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Eukaryota; Metazoa; Chordata; Cran
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WIEDVMK 804
                                                                                                                                                                                                                                                                       CAGHLVG--RGDSCQGDSGGPLIC-FEDDKYVLQGVTSWGLGCARPNKPGVYVRVSRYIS
                                                                                                                                                                                                    I 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV
                                                 CAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVP
                                                                                                              LPLWRERPQKTASNCYITGWGDTGRAYSRTL-QQAAIPLLPKRFCEER-Y-KGRFTGRML
                                                                                                                                   LP-SQDFWVPDRTLCHVTGWGDTQGTSPRGLLKQASLPVIDNRVCNRHEYLNGRVKSTEL
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l Similarity 40.9%;
l01; Conservation
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05, Last sequence update)
12, Last annotation update)
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Pred. No. 3.93e-106;
39; Mismatches 90;
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RESULT 12
O16618
ID O16618
AC O16618
D7 01-NOV-1996 (TIEMBLrel. 01, Created)
D7 01-NOV-1996 (TIEMBLrel. 01, Last sequence update)
D7 01-NOV-1999 (TIEMBLrel. 11, Last annotation update)
D7 01-NOV-1999 (TIEMBLrel. 12, Last annotation update)
D8 UROKINASE PRECURSOR (EC 3.4.99.26).

GN HOMO Sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; 1
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RN SEQUENCE FROM N.A.
RX MEDLINE; 85203359.
RX MOICCLIAR CIONING; Sequencing, and expression in Eschuman preprourokinase cDNA.";
RT MOICCLIAR CIONING; Sequencing, and expression in Eschuman preprourokinase cDNA.";
DNA 4:139-146(1985).
DR EMBL; WO2760; CAA26535.1; -.
DR HSSP; P00749; 1URK.
DR FFAM; PF00089; tripgin; 1.
DR PFAM; PF00089; tripgin; 1.
DR PFAM; PF00089; tripgin; 1.
DR PFAM; PF00072; CHYMOTRYPSIN.
KY Signal; Serine protease.
FT SIGNAL 1 20 UROKINASE.
SEQUENCE 431 AA; 48664 MW; 9B8C8D5F CRC32;
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Best Local S
Matches
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097506;
097506;
01-MAY-1999
01-MAY-1999
                                                                                            Sus scrofa (Pig).
Sus scrofa; Metazoa; Chordata; Craniata; V.
Eukaryota; Metazoa; Chordata; Suina; Suidae;
TAKAHASHI T., KIMURA A., OKIMURA H., HAMABATA T.; "Porcine liver plasma kallikrein."; submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                     SEQUENCE FROM N.A.
                                                                                                                                                          KALLIKREIN
                                                      rissue=plasma;
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Similarity 36.5%;
92; Conservative
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Last annotation updat
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Pred. No. 4.88e-103;
                                                                                                                                                                                                                                                   643
                                                                                                         Vertebrata;
e; Sus.
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DAVIES B.J., PICKARD B.S., STEEL M., MORRIS R.G., "Serine proteases in rodent hippocampus.";
J. Biol. Chem. 273:23004-23011(1998).

EMBL; AJ005642; CAA06644.1; -.
HSSP; P00763; 1DPO.
PFAM; PF00089; trypsin; 1.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE PROTEASE PRECURSOR (FRAGMENT).
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                                                                                           697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 IVGGTDSELGEWPWQVSLQAKL-RAQNHL-CGGSIIGHQWVLTAAHCFDGLSLPDIWRIY 456 | |-|| |-|| |-|| |-|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--|| |--||
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                                                                                                                                                                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 VVGGEDSADAQWPWIVSI-LK--NG-SHH-CAGSLLINRWVVSAAHCFSSNMDKPSPYSV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
AITEDMLCAGYL-EGKR-DACLGDSGGPLMCQ-VDDHWLLTGIISWGEGCAERNRPGVYT
                                                                                   CLPLWRERPQKTASNCYITGWGDT--GRAYSR--TLQQAAIPLLPKRFCEERY-KG--R-
                                                                                                                                                                                                                                                         RVGDYHTLVPEEFEEEIGVQQIVIHREY-RPDRSDYDIALVRLQGPEEQCARFSSHVLPA 696
                                                                                                                                                                                                                                                                                                     LLGAWKLGNPGPRSQKVGIASVLPHPRYSRKEGTHADIALVRLERPI-Q---FSERILPI 150
                                                                                                                                                                                                                                                                                                                                                                                                                           MUWI
                                                                                                                                                                      CLPDSSVHLP-PNTNCWIAGWGSIQDGVPLPRPQTLQKLKVPIIDPELCKSLYWRGAGQE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGILNISEITKETPFSQ----VKEIIIHQNYKILESGHDIALLKLETPLN-YTDF--QK-P 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MICAGY-KEGGK-DACKGESGGPLVCKYNGI-WHLVGTTSWGEGCARREQPGVYTKVIEY 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICLP-SRDDTNVVYTNCWVTGWGFTEEKGEIQNILQKVNIPLVSNEECQKSYRDHKISKQ 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACLPLWRERPQKTASNCYITGWGDTG-RA-YSRTLQQAAIPLLPKRFCEERYKG-RFTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 27.4%;
Similarity 38.1%;
96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
92; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Metazoa; Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72227 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
53; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 518; DB 11;
Pred. No. 5.98e-100;
53; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 530; DB 6; L
Pred. No. 4.88e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
SERINE PROTEASE.
; 1B072619 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F0154450 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LATHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                637
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RESULT 15
ID 091674
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                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                      CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U44951; AAA91466.1; -. HSSP; P00763; 1DPO. PFAM; PF00431; CUB; 5. PFAM; PF00089; trypsin; 3. PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1273-1524 FROM N.A.
YANG J.C., HEDRICK J.L.;
Submitted (DEC-1955) to the EMBL/GenBank/DDBJ
EMBL; U81290; AAC24717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
YANG J.C., LINDSAY L.L., HEDRICK J.L.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYPROTEIN (OVOCHYMASE). • Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus.
                                                                                                                                                                                                                                                                                                                                                                            Polyprote:
814
                        810
                                                   754
                                                                             751
                                                                                                       697
                                                                                                                                692
                                                                                                                                                           637
                                                                                                                                                                                                                                        584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    808 KVSAFVPWIKSV 819
PWIKS
                        TWION
                                                                            LCAG-FPSSKEKDACQGDSGGPLVCQNEKEQFSIYGLVSWGEGCGRVSKPGVYTKVRLFF
                                                                                                     CLPLWRERPQKTASNCYITGWGDTGR-AYSR-TLQQAAIPLLPKRFCEERY-KGRFTGRM
                                                                                                                         CLPE-PEEVLTPASVCVVTGWGNTAEDGQPALGLQQLQLPILDSIICNTSYYSGELTDHM
                                                                                                                                                                                                              IIGGKNSLRGGWPWQVSLR-LKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYA
                                                                                                                                                                                                                                       IVGGEEASPNSWPWQVQIFFLRTFH-----CEGAIISPQWILTAAHCI-RAAEPS-YWT
                                                   LCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFV
                                                                                                                                                         VRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPA 696
                                                                                                                                                                                 VIAGDHNRMLNESTEQIRNIKTIRIHDNYNSETYDNDIALLYLEEPLDL-NDF---VRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLLAHRPWVQRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -FTGRMICAGNIHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYT
                                                                                                                                                                                                                                                                h 27.1%;
Similarity 39.2%;
96; Conservative
818
                        814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 (TremBLrel. 01, C
B (TremBLrel. 08, I
9 (TremBLrel. 12, I
N (OVOCHYMASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                       AA,
                                                                                                                                                                                                                                                                                                                                  308
817
1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278
                                                                                                                                                                                                                                                                                                                      24 OVOCHYMASE
167566 MW; 40D9670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                Score 512; DB 13; I
Pred. No. 2.08e-98;
48; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                SERINE PROTEASE
SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                       40D967CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        databases
                                                                                                                                                                                                                                                                                         Length 1524;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                  18;
                                                   813
                                                                                                      753
                                                                                                                                                                                                              636
                                                                                                                                                                                                                                        635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       807
```

Title: Description: Perfect Score: Sequence: Tabular output not generated. ************************ Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Mon Mar 13 10:19:00 2000; MasPar time 12.76 Seconds 454.820 Million cell updates/sec ************* (MT)

>US-09-147-947-6 (578-822) from US09147947A.pep (1 of 6) 1892 1 IIGGKNSLRGGWPWQVSLRL......PGVYTKVSAFVPWIKSVTKL 245

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 32.789; Variance 126.286; scale 0.260

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Query Match	Length	DB	Ħ	Description	Pred. No.
ш.	1892	100.0	822		W99087	Human serine protease	9e-19
2	1892		875	٢	336	neurotrypsin.	. 99
ω	1752		761	μ	$\frac{3}{3}$		3e-17
4	1752	92.6	761	<u>,</u>	88066M	Mouse serine protease	7
υ	561	9.	522	↦	R13921	~	.36e-4
σ	559	٩	522	ы	R13920	Delta (466-470) tPA va	.23e-4
7	554	9	356	μ.	W46917	no acid sequence o	.65e-4
œ	553	9	395	ப	R47902	deriva	.78e-4
•	552	9	434	Н	R13922		.25e-4
10	553	9	522	س	R13918	0) tE	.78e-4
11	552	9	522	ب	R14486		.25e-4
12	551	9	412	سر	-	UK-S1 as encoded by pS	.60e-4
ω	551	9	522	-	R13919	(466-470) tPA	.60e-4
14	548	9	378	-	w	a	.35e-4
15	54.80	9	389	٢	W13636	Human prourokinase var	.35e-4
16	548	29.0	401	سا	w	Human prourokinase var	3.35e-45
17	548	9	411	Н	63	tive prourc	.35e-4
18	548	9	411	Н	R47958	PUK S26T.	.35e-4
19	548	9	411	ب	95	PUK C32P.	.35e-4
20	548	9	411	ш	R47963	PUK G53A.	.35e-4
21	548	9	411	سر	R47964	PUK N32P G38K.	5e-4
22	548	9.	411	۲	R47957	PUK Y24A.	.35e-4
23	548	9	411	11	R40225	PUK.	5e-4

45	44	43	42	41	40	39	38	37	36	ა 5	34	33	32	31	30	29	28	27	26	25	24
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3	Non-glycosylated prour	Inhibitor resistant ur	Recombinant single-cha	Sequence of human pro-	Pro-urokinase mutant G	Pro-urokinase mutant S	Pro-urokinase mutant S	Plasminogen activator	Sequence of mutants of	[GARSYQ]-[Plasminogen	JM1-229 cell line t-PA	Pro-urokinase mutant S	Pro-urokinase mutant H	Pro-urokinase mutant S	PUK G38A G39A.	PUK G38A.	Pro-urokinase mutant S	PUK G16A G17A.	PUK N32P G38K G39K.	PUK P34A.	PUK G16A.
7.00e-45	7.00e-45		8.95e-45	8.95e-45	8.95e-45	8.95e-45	7.00e-45	4	4	7.00e-45	5.47e-45	4.28e-45	4		3.35e-45	٠		3.35e-45	3.35e-45	3.35e-45	3.35e-45

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Db 818 SVTKL 822	Qy 758 NLHEHKRVDSCQGDSGGPLMCER	Db 758 NLHEHKRVDSCOGDSGGPLMCER	Qy 698 LPLWRERPQKTASNCYITGWGDT	Db 698 LPLWRERPQKTASNCYITGWGDT	Qy 638 RVGDYHTLVPEEFEEEIGVQQIV	Db 638 RVGDYHTLVPEEFEEEIGVQQIV	Qy 578 IIGGKNSLRGGWPWQVSLRLKSS	Db 578 IIGGKNSLRGGWPWQVSLRLKSS	Query Match 100.0%; Best Local Similarity 100.0%; Matches 245; Conservative		CC sprine protease inhihitors of			The present sequence	for potential serine	New serine protease		wpr. 99-142942712	ORY LTD.			PD 04-FEB-1999	DN W09905290-A1	Serine protease; BSSP-3; br	Human serine	DT 13-MAV-1999 (first ontry)	W99087 standard; Protein;	RESULT 1
	NLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK 817	NLHEHKRVDSCOGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK 817	LPLWRERPQKTASNCYITGWGDTGRAYSRTLQQAAIPLLPKRFCEERYKGRFTGRMLCAG 757	LPLWRERPQKTASNCYITGWGDTGRAYSRTLQQAAIPLLPKRFCEERYKGRFTGRMLCAG 757	RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPAC 697	VIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPAC 697	IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV 637	SHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV 637	Score 1892; DB 1; Length 822; Pred. No. 9.99e-193; 0; Mismatches 0; Indels 0; Gaps 0;	or expression regulations for use as unitys.	invention are used for screening for potential peptide or non-peptide	artial sequences. Products from the present	isolated from human brain tissue. Transformants may be used to	is a serine protease designated BSSD-3, which	se inhibitors for drug use	ed in brain tissue - used in screening		ramasniro k;						ain tissue.	ω.		822 AA.	

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Claim 1; page 20-24; 50pp; English.

Claim 1; page 20-24; 50pp; English.

The present sequence represents human neurotrypsin. Neurotrypsin proteins and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or retina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration, neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to increase survival of damaged neurons (e.g. in cases of hypoxia, cases of increase survival of damaged neurons (e.g. in cases of hypoxia, cases of cell death) in the neurous system; (vii) to regenerate brain causes of cell death) in the nervous system; (vii) to regenerate brain performance, including learning and memory; (x) to treat or prevent a cand/or lang-verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders; and (xi) to treat brain or lung verse of psychiatric disorders.
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W83362 standard;
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26-APR-1997; CH-000966.
SOND/) SONDEREGGER P.
onderegger P:
pI; 99-009438/01.
N-PSDB; V72589.
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WO9849322-A1.
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Schaim 1; Page 29-32; Sopp; English.

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04-FEB-1999.
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24-JUL-1997;
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W09905290-A1
                                                                                                                                                                      Serine protease;
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                                                                                                                                                                                                            Mouse serine
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WO9849322-A1.
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26-APR-1997; CH-000966.
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                                                                                                                                                                                                         BSSP-3
                                                                                                                                                                                                                                                                                                               761
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Pred. No. 3.43e-177;
17; Mismatches 8;
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e sclerosis;
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Best Local
                                                                                                   Matches
                                                                                                                                                                                vascular disease, embolism etc.
Claim 5; Page 27; 33pp; English.
This tPA variant has a deletion of amino acids Pro(466) to Leu(470) of the corresponding wild-type. It also has amino acids 432 and 434 substituted by Ala residues. The deletion is in the serine protease domain, making the variant more fibrin specific than the wild-type tPA. See R13917-R13922 and r14486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; X19027.

New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Example 1; Page 51-54; 69pp; Japanese.

The present sequence is a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs.
                                                                                                                                                                                                                                                                                                New tissue plasminogen activator variant used for vascular conditions - e.g. to prevent fibrin deposition or adhesion formation or reformation, deep vein thrombosis, peripheral
                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
Gill JF, Presta LG, Zoller
WPI; 91-281468/38.
                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-1991.
14-FEB-1991; U01025.
01-MAR-1990; US-486657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue plasminogen activator; WO9113149-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27\text{-NOV-}1991 (first entry) Delta (466-470) tPA variant with H432A and R434A substns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R13921 standard; Protein; 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUNR ) SUNTORY LTD.
TSuruoka N, Yamaguchi N,
WPI; 99-142942/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1991
345
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                                                                  288
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                                                  PWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERF--PPHHLTVILGRTYR-VV 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVGDYHTLVPEEFEQEIGVQQIVIHRNYRPDRSDYDIALVRLQGPGEQCARLSTHVLPAC 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVTKL
PGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPP-ADLQL 403
                             SVTSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLQEDNRVDSCQGDSGGFLMCEKPDESWVVYGVTSWGYGCGVKDTPGVYTRVPAFVPWIK 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPAC
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220; Conser
                                                                                                Similarity 40.3%;
95; Conservative
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Pred. No. 3.43e-177;
17; Mismatches 8;
                                                                                                Score 561; DB 1; Le
Pred. No. 1.36e-46;
52; Mismatches 75;
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Best Local
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01-MAR-1990; US-48657.
(GETH ) GENENTECH INC.
G111 JF, Presta LG, Z0114
WPI; 91-281468/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tissue plasminogen activator variant used for vascular conditions - e.g. to prevent fibrin deposition or adhesion formation or reformation, deep vein thrombosis, peripheral vascular disease, embolism etc.

Claim 5; Page 27; 33pp; English.

This tpA variant has a deletion of amino acids Pro(466) to Leu(470) of the corresponding wild-type. It also has amino acids 339 and 342 substituted by Ala residues. The deletion is in the serine protease domain, making the variant more fibrin specific than the wild-type tpA. See R13917-R13922 and R14486.
                                                                                                                                                                                                                                                                                     02-JUL-1998 (first entry)
Amino acid sequence of a novel human kallikrein.
Kallikrein; HKLP; human; serine protease; drug screening; agonist; treatment; hypertension; cardiac hypertrophy; art inflammatory disorder; blood clotting disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W46917 standard; Peptide; W46917;
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R13920;
                                                                                  Misc_difference
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05-SEP-1991.
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Delta (466-470) tPA variant with R339A and R342A substns
                                                                                                                                                                    Misc_difference
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Similarity 39.6%;
93; Conservation
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                                                                                                                                                                Location/Qualifiers
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21-JUL-1997;
22-JUL-1996;
high thrombolytic activity, useful for to bisclosure; Page 14; 29pp; Japanese. Sequences (Q5571-72) are pro-urokinase have an inserted sugar moeity having an
                                                                                                                                                                     21-DEC-1993.
17-OCT-1991; 269615.
17-OCT-1991; JP-269615.
(KYOW) KYOWA HAKKO KOGYO KK.
WPI: 94-030907/04.
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T Bandman O, Braxton
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                                                                                  human pro-urokinase derivs. having long half-life thrombolytic activity, useful for treatment of thro
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1. No. 7.65e-46;
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                           vascular disease, embolism etc.
Claim 12; Page 27; 33pp; English.
This tPA variant has a delation of amino acids Pro(466) to Leu of the corresponding wild-type. The deletion is in the serine protease domain, making the variant more fibrin specific than wild-type tPA. The variant also has a deletion of amino acids Cys(92) to Asp(179) of the wild-type sequence (i.e. Kringle 1 domain). See also R13917-R13921 and R14486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tissue plasminogen activator variant used conditions - e.g. to prevent fibrin deposition formation or reformation, deep vein thrombosis
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Gill JF, Presta LG, Zo
WPI; 91-281468/38.
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                                                                                                                                                                                                                                        Local Similarity
nes 94; Consen
                                                                                                                                               PWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERF--PPHHLTVILGRTYR-VV 256
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     PEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQ
                                                           PGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPP-ADLQL 315
                                                                                                                    PWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHCFK-RYGNSTRSYAVRVG-DYHTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAFVPWIKSVTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACLP-LWRERPOKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV
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Similarity 37.3%;
94; Conservative
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                                                                                                                                                                                                                                  Score 552; DB 1;
Pred. No. 1.25e-45;
51; Mismatches 77
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60; M
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No. 9.78e-46;
Mismatches 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          riant used for vascular deposition or adhesion thrombosis, peripheral
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                                                                                                                                                                                                                                                                                              Length 434;
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Matches
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Delta (466-470) tPA variant with K416A, H417A and E41
tissue plasminogen activator; infarction; coagulation
W09113149-A.
05-SEP-1991.
05-SEP-1991.
01-MAR-1990; US-486657.
(GETH ) GENENTECH INC.
Gill JF, Presta LG, Zoller ML;
WPI; 91-281468/38.
                                                                                                                                                                                                                                                                                                                                                                                                                      R14486 standa
R14486;
R14486;
27-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tissue plasminogen activator variant used for vascular conditions - e.g. to prevent fibrin deposition or adhesion formation or reformation, deep vein thrombosis, peripheral vascular disease, embolism etc. Claim 5; Page 27; 33pp; English. This tPA variant has a deletion of amino acids Pro(466) to Leu(470) of the corresponding wild-type. It also has amino acids 416 to 418 substituted by Ala residues. The deletion is in the serine protease domain, making the variant more fibrin specific than the wild-type tPA. See R13917-R13922 and R14486.
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R13918
R13918;
05-SEP-1991.
14-FEB-1991; U01025.
01-MAR-1990; US-486657
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                             (466-470) tPA variant with Y67N substitution
plasminogen activator; infarction; coagulat:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                   /label= Kringle
180. .261
/label= Kringle
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Pred. No. 9.78e-46;
51; Mismatches 77;
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Best Local
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28-SEP-1989;
29-SEP-1989;
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WPI, 91-281468/38.
New tissue plasminogen activator variant used for conditions - e.g. to prevent fibrin deposition of formation or reformation, deep vein thrombosis, embolism etc.
                                                                                                                                                                                                                                             physiochemical properties.

Disclosure; 30pp; English.

The polypeptide is a deriv. of mature urokinase, design UK-S1 which has an amino acid substn. which results in UK-S1 which has again the new protein improved stak
                                                                                                                                                                                                                                                                                                                                                                            Polypeptide(s) with added carbohydrate chains modification of amino acid sequence, used to i physiochemical properties and/or activities.
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R05116 standard; protein;
R05116;
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Claim 11; Page 27; 33pp; English.

This tPA variant has a deletion of amino acids Pro(466) to Leu(470) of the corresponding wild-type. It also has amino acids 57 (Tyr) substituted by an Asn residue to create a glycosylation site. The deletion is in the serine protease domain, making the variant more fibrin specific than the wild-type tPA. See also R13917-R13922.
                                                                                                                                                                                                        sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Q04485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOW) Kyowa Hakka KK.
Sasaki K, Nishi T, Yasumuru S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-1990 (first entry)
UK-S1 as encoded by pSEIUKS11d
Urokinase; glycosylation.
                                                                                                                                                                                                                                   See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP-370205-A.
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                                               IIGGENTTIENQPWFAAIYRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKE-DYIV 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK
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94; Conser
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Similarity 39.8%;
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412 AA;
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larity 37.3%;
Conservative
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JP-245705.
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/note="old seq (Phe)"
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Pred.
60; M
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Pred. No. 1.25e-
51; Mismatches
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1. No. 1.60e-45;
1. matches 84;
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cches 77;
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on or adhesion
is, peripheral
                                                                                                                                                    Length 412;
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Best Local :
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   Synthetic
                 epidermal growth Homo sapiens.
                                            Human prourokinase variant lacking entire EGF domain. Human; prourokinase; hPUK; variant; half-life; increa
                                                                           04-JUN-1997
                                                                                           W13635 standard;
W13635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wild-type tPA.
Sequence 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vascular disease, embolism etc.
Claim 5: Page 27: 33pp; English.
This tPA variant has a deletion of amino acids Pro(466) to Leu(470)
of the corresponding wild-type. It also has amino acids 426-7 and
429-430 substituted by Ala residues. The deletion is in the serine
protease domain, making the variant more fibrin specific than the
wild-type tPA. See R13917-R13922 and R14486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tissue plasminogen activator variant used for vascular conditions - e.g. to prevent fibrin deposition or adhesion formation or reformation, deep vein thrombosis, peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gill JF, Presta LOWPI; 91-281468/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-FEB-1991; U01025.
01-MAR-1990; US-486657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue plasminogen activator; infarction; coagulation
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                                                                                                                                                                      HKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK
                                                                                                                                                                                      GGH-DACQGDSGGPLVCLNDGRMTLV-GIISWGLGCGQKDVPGVYTKVTNYLDWIR 517
                                                                                                                                                                                                                                                                                                              PGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPP-ADLQL 403
                                                                                                                                                                                                                                 KTASNCYITGWG--DT-GRAYSRTLQQAAIPLLPKRFC-EERYKGR-FTGRMLCAGNLHE
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                                                                                                                                                                                                                                                                                            PEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 standard; Protein; 522
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Similarity 39.88;
94; Conservation
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                              factor
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                                                                            entry)
                               domain;
                                                                                                           378
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 551; DB 1; Lo
Pred. No. 1.60e-45;
51; Mismatches 77;
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                              deletion;
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                              thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 522;
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                                              increase;
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                              fibrinolysis
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Best Local s
Matches 9
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18-MAY-1989; JP-126433.
22-FEB-1990; JP-042020.
(GREC ) GREEN CROSS CORP.
Airmura H, Amatsuji Y, H
Morita M, Tanabe T;
WPI; 90-350146/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page ; 22pp; English.

New variants of human prourokinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain; (ii) at least part of the first loop and at least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while retaining the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause spontaneous bleeding. The present sequence represents a specific variant of the whole hacks the entire EGF domain; the sequence does not
              Human prourokinase variant lacking EGF domain loops 1 and Human; prourokinase; hPUK; variant; half-life; increase; epidermal growth factor domain; deletion; thrombolysis; fi
                                                                           IT 15
W13636 standard;
W13636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     appear in the specification and has been created using the wild-type hPUK sequence and the junction sequence after deletion, both of which are given (in Fig 1 and in Fig 2(3),
                                                             04-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          respectively).
Sequence 378
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18-FEB-1987; JP-036495.
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18-MAY-1990;
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                                                                                                                                                                                                                                                                                                         ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV
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                                                                                                                                                                                                                                                                                                                                                                     YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 244
                                                                                                                                                                                                                                                                                                                                                                                                   IIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAV 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
93; Conse
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larity 36.9%;
Conservative
                                                             (first entry)
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                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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Pred.
60; M
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No. 3.35e-45;
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               life; increase; EGF;
thrombolysis; fibrinolysis
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Best Local Similarity 36.9%;
Matches 93; Conservative
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18-MAY-1989; JP-126433.
22-FER-1990; JP-042020.
(GREC 'GREEN CROSS CORP.
Airmura H. Amatsuji Y. Hi
Morita M. Tanabe T;
WPI; 90-350146/47.
N-PSDB; T61673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variants of human prourokinase (hPUK) comprise a hPUK deficient in (i) at least part of the first loop region of the epidermal growth factor (EGF) domain; (ii) at least part of the first loop and at least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while retaining the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause spontaneous bleeding. The present sequence represents a specific variant of hPUK which lacks loops 1 and 2 of the EGF domain; the sequence does not appear in the specification and has been created using the wild-type hPUK sequence and the junction sequence after deletion, both of which are given (in Fig 1 and on page 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respectively).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as
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New variants of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-1990.
18-MAY-1990; 109472.
03-JUL-1986; JP-156936.
18-FEB-1987; JP-036495.
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                                                                                                                                                                                                                                                                                                                                                                                                                137 IIGGEFTTIENOPWFAAITRRHRGGSVTYVCGGSLISPCWVISATHCFIDYPKKE-DYIV 195
    810 SAFVPWIKSVTK 821
                                             371 SHFLPWIRSHTK 382
                                                                                                                         314 TTKMLCAAD-PQWK-TDSCQGDSGGPLVCSLQGRM-TLTGIVSWGRGCALKDKPGVYTRV 370
                                                                                                                                                                                  696 ACLP-LWRERPQKTASNCYITGWG-DTGRAY--SRTLQQAAIPLLPKRFCEE-RYKGR-F 749
                                                                                                                                                                                                                 256 ICLPSMYND-PQ-FGTSCEITGFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYYGSEV 313
                                                                                                                                                                                                                                                                          638 RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDR-SDY-DIALVRLQGPEEQCARFSSHVLP 695
                                                                                                                                                                                                                                                                                                                        196 YLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ibrinolytic agent
                                                                                          750 TGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKV 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "residues 33-411 of native hPUK" 155
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11. .389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 548; DB 1; Le Pred. No. 3.35e-45; 60; Mismatches 85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Search completed: Mon Mar 13 10:19:14 2000 Job time : 14 secs.

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********************** dd_u Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm

(MT)

Run on: Mon Mar 13 10:18:23 2000; MasPar time 18.79 Seconds 615.076 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence:

>US-09-147-947-6 (578-822) from US09147947A.pep (1 of 6) 1892 1 IIGGKNSLRGGWPWQVSLRL......PGVYTKVSAFVPWIKSVTKL 245

Searched: PAM 150 Gap 11 142080 segs, 47172406 residues

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 44.068; Variance 74.731; scale 0.590

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20 514 21 512																				•		t Score
27.1		7	7.	7.	7.	28.3	8	8	8	8	8	œ	9	9	9	0	1	1.	1	33.0		Query Match
477																						Length DB
1 A34369 2 A61545	UKBAY		2 JC5878	1 UKHUT			JE031			S2959		JX017	S4753						1 KQMSPL	1 KFHU1	2 JC5759	B ID
t-plasminogen activat plasmin (EC 3.4.21.7)	acti	crosin (EC 3.4.21	ō.	en a	t-plasminogen activat	plasmin (EC 3.4.21.7)	low-density lipoprote	uro	n activa	.4.21.1	n activa	3.4.	(EC 3.4.	(EC 3.4.2	acrosin (EC 3.4.21.10	4.21.	.ikrein (lasma kallikre	ikrein (ation factor	brain-specific serine	Description
4.	7.23e-90	.45e-	.30e-9	.14e-9	.14e-9	.61e-9	.19e-	.07e-9	.21e-9	.21e-9	.03e-9	. 086	. 246	. 766	٠.	. 656	.92e-10		.09e-11		0.00e+00	Pred. No.

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	plasmin (EC 3.4.21.7)	enteropeptidase (EC 3	hypothetical protein	coagulation factor XI	u-plasminogen activat	complement C3b/C4b in	chymotrypsin-like pro	plasmin (EC 3.4.21.7)	u-plasminogen activat	plasmin (EC 3.4.21.7)	plasmin (EC 3.4.21.7)	u-plasminogen activat		activat	activat		t-plasminogen activat	enteropeptidase (EC 3	plasmin (EC 3.4.21.7)	plasmin (EC 3.4.21.7)	u-plasminogen activat	hepatocyte growth fac	
	2.09e-78	2.45e-79	4.90e-80	1.67e-80	1.67e-80	5.72e-81	5.72e-81	1.95e-81	1.33e-82	2.64e-83	5.25e-84	1.79e-84	8.13e-87	8.13e-87	8.13e-87	8.13e-87	2.76e-87	9.38e-88	9.38e-88	5.47e-88	5.47e-88	3.18e-88	•

ALIGNMENTS

RVGDYHTLVPEEFEQEIGVQQIVIHRNYRPDRSDYDIALVRLQGPGEQCARLSTHVLPAC 636	577	Db
IIGGNNSLRGAWPWQASLRLRSAHGDGRLLCGATLLSSCWVLTAAHCFKRYGNNSRSYAV 576 : : : :	517 578	QQ Qy
h 92.6%; Score 1752; DB 2; Length 761; Similarity 89.8%; Pred. No. 0.00e+00; 220; Conservative 17; Mismatches 8; Indels 0; Gaps 0;	Query Match Best Local Similarity Matches 220; Conse	
predicted\ #active_site His, Asp, Ser #status predicted #length 761 #molecular-weight 84136 #checksum 5449	562,612,711 SUMMARY	ຜ
<pre>#domain furin binding #status predicted #label FRB\ #domain trypsin homology #label TRY\ #binding_site carbohydrate (Asn) (covalent) #status</pre>	513-516 517-755 93,521,569	
#domain scavenger receptor cysteine-rich #status predicted #label SRC\	100-200,2/3-3/2, 386-486	
#domain kringle-like #status predicted #label KRI\ #domain scavenger receptor cysteine-rich domain homology #label SRC7\	85-157 163-266	
cysteine-rich domain nomology glycoprotein; hydrolase; serine proteinase	KEYWORDS	чχ
##ccross-relerences DDBJ:D898/1 ##experimental_source brain FICATION #superfamily_trypsin_homology; scavenger_receptor	##cross-1 ##experin CLASSIFICATION	C
##molecule_type mRNA ##residues 1-761 ##label YAM	##residue	
JC5759	#accession	
ysteine-rich motifs.	#cross-references	
	#title	
Tsujimura, A.; Yamaguchi, N. Biochem. Biophys. Res. Commun. (1997) 239:386-392	#journal	
Yamamura, Y.; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.;	#authors	
JC5759 JC5759	ACCESSIONS REFERENCE	r Þ
<pre>24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999</pre>	DATE	D
#formal_name Mus musculus #common_name house mouse	ORGANISM	O H
JC5759 #type complete	ENTRY	3 tx
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#journal
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                                                                       #map_position
#introns
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#title Amino acid sequence of human factor XI, a blood coagulation factor with four tandem repeats that are highly homologous #cross-references MUID:86243360

#accession A00920
    #description
                                                                                                                                       #gene
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#journal Biochemistry (1987) 26:7221-7228
#title Organization of the gene for hum
#cross-references_MUID:88107663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #accession
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                                             ##cross-references GDB:119891; OMIM:264900
ag_position 4q35-4q35
ntrons 19/1; 73/2; 109/1; 162/2; 199/1;
435/2; 494/1; 526/1; 572/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-625 ##label FUJ
##cross-references GB:M13142; NID:g182832; PIDN:AAA52487.1;
NCE A37940
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##residues 1-625 ##label ASA
##cross-references GB:M18295
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                                                                                                                                                                                                                                                                          The
                                                                                                                                                                              he proenzyme consists of two identical chains linked by one or more disulfide bonds. It is activated by factor XIIa (or XII), which cleaves each chain into a light chain, which contains th active site, and a heavy chain, which associates with high molecular weight (HMW) kininogen.
catalyzes the proteolytic activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A37940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McMullen, B.A.; Fujikawa, K.; Davie, E.W. Biochemistry (1991) 30:2056-2060 Location of the disulfide bonds in human oc XI: the presence of tandem apple domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coagulation factor Xia (EC 3.4.21.27) precursor - human antihemophilic factor C; plasma thromboplastin antecedent #formal_name Homo sapiens #common_name man 13-Aug-1986 #sequence_revision 26-May-1994 #text_change
                                                                                                                                       GDB:F11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A00920
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A27431
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28-33:35-49, 'x', 51-55, 'x', 57-63:70-75, 'x', 77-79:107-109, 'X', 111-112;132-139; 'X', 1141-154;163-164, 'x', 1166-168; 'X', 111-112;132-139; 'X', 123-228;229, 'X', 231-225, 'X', 192, 'X', 194;198-199, 'X';223-228;229, 'X', 231-225, 'X', 237-248;253-254, 'X', 256-258;280-282, 'X', 284;285-297; 313-316, 'X', 318-319;320-326; 'X', 328-330; 'X', 347-349; 373, 'X', 375;377-379, 'X', 381-383;414-415, 'X', 417-431, 'X', 433-437;486-499, 'X', 501-507;535-548;559, 'X', 561-564 ##label MCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the sequence shown follows the authors' translation
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CLASSIFICATION
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416-432,545-560
90,126,353,450
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140-146,200-283,
226-255,230-236,
291-374,317-346,
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387-388
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109-198
199-288
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491
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20-103,514-581,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                    MICAGY-REGGK-DACKGDSGGPLSC-KHNEVWHLVGITSWGEGCAQRERPGVYTNVVEY 614
                                                                                                                                                                                                                           ω
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                                                                                                                                                                                                                                                                                                                                                    MLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICLPSKGDR-NVIYTDCWVTGWGYRKLRDKIQNTLQKAKIPLVTNEECQKRYRGHKITHK 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRVGD-YHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102;
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Similarity 41.8%;
                                                                                                                                                                                                                                                                               816
                                                                                                                                                                                                                                                                                                                  618
                                                                                                             A36557
                                                                                                                            KOMSPL #type complete
plasma kallikrein (EC 3.4.21.34) precursor -
#formal_name Mus musculus #common_name house
30-sep-1992 #sequence_revision 30-sep-1992 #t
18-Jun-1999
G.; Brachpapa, L.; Rochemont, J.; Mbika DNA Cell Biol. (1990) 9:737-748
Mouse plasma kallikrein: cDNA structure, characterization, and comparison of pro
                                                                          Seidah, N.G.; Sawyer, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #length 625
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#domain apple repeat #label AP3\
#domain apple repeat #label AP4\
#domain apple repeat #label AP4\
#product coagulation factor XIa light
experimental #label LCH\
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#binding_site_carbohydrate
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#binding_site carbohydrate (Asn) (cova predicted\
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#cleavage_site Arg-Ile (coagulation factor XII
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#disulfide_bonds interchain #status
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Pred. No. 1.
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                                                    Hamelin, J.; Mion emont, J.; Mbikay,
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SUMMARY
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141-147,201-284,
227-256,231-237,
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383-503,419-435,
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RDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 IVGGTNASLGEWPWQVSLQVKLV-SQTHL-CGGSIIGRQWVLTAAHCFDGIPYPDVWRIY 448
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##note part of this sequence, including the amino ends of both
the heavy and light chains, was confirmed by protein
                                                                                                                                                                  618 MDWI 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incal Similarity 40.68; les 99; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLP
                                                                                                                                                                                                                                                         MICAGY-KEGG-TDACKGDSGGPLVCKHSG-RWQLVGITSWGEGCGRKDQPGVYTKVSEY 617
                                                                                                                                                                                                                                                                                                       ACLPLWRERPQKTASNCYITGWGDT-GRAYSRT-LQQAAIPLLPKRFCEERYKGRFTGR-
                                                                                                                                                                                                                                                                                                                                                   ICLP-SKADTNTIYTNCWVTGWGYTKEQGETQNILQKATIPLVPNEECQKKYRDYVINKQ 560
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGILS-L-SEITKETPSSR-IKELIIHQEYKVSEGNYDIALIKLQTPLN-YTEF--QK-P 501
                                                                                                                                                                                                                MLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAF 812
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linked by one or more disulfide bonds.
DN #superfamily coagulation factor XI; trypsin homology
blood coagulation; duplication; fibrinolysis; glycoprotein;
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th 638 #molecular-wei
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#domain apple repeat #label AP2\
#domain apple repeat #label AP3\
#domain apple repeat #label AP4\
#domain apple repeat #label AP4\
#product plasma kallikrein light chain #status
experimental #label LCH\
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#type complete
kallikrein (EC 3.4.21.34)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 600; DB 1; L
Pred. No. 1.09e-110;
54; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps 16;
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FEATURE
1-19
                                                                                                                                                                                                                                                                                                                             #gene
CLASSIFICATION
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  20-109
110-199
200-289
291-380
391-638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal Biochim. Biophys. Acta (1989) 999:103-110
Rat plasma kallikrein: purification, NH(2)-terminal
#title sequencing and development of a specific radioimmunoassay.
#cross-references MUID:90089457
                                                                                                                                                                 20-390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal
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**authors Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Ham Lutfalla, G.; Rougeon, F.; Lazure, C.; Chr

**journal DNA (1989) 8:563-574

**title The CDNA structure of rat plasma kallikrein.

**cross-references MUID:90091743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
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#accession A39180
                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-638 ##label RES

##cross-references GB:MS8590; NID:9206721; PIDN:AAA42069.1; PID:9206722

NT This protein, synthesized in the liver, circulates as a noncovalent complex with high molecular weight (HMW) kininogen.

NT The zymogen is activated by factor XIIa, which cleaves the molecule into a light chain, which contains the active site, and a heavy chain, which associates with HMW kininogen. These chains are linked by one or more disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type protein
##residues 20-45;391-413 ##label PAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **status not compared with ##molecule_type mRNA
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##cross-references GB:J05315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seidah, N.G.; Ladenheim, R.; Mbikay, M.; Ham
Lutfâlla, G.; Rougeon, R.; Lazure, C.; Chr
DNA Cell Biol. (1989) 8:563-574
The cDNA structure of rat plasma kallikrein.
                                                                                                                                                                                                                                                                 #superfamily coagulation factor XI; trypsin homology blood coagulation; duplication; fibrinolysis; glycop hydrolase; inflammation; liver; plasma; serine pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S06851
Paquin, J.; Benjannet, S.; Sawyer, N.; Lazure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chretien, M.; Seidah, N.G.
Biochemistry (1991) 30:1628-1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fletcher factor; kininogenin; serum kallikrein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beaubien, G.; Rosinski-Chupin, I.; Mattei, M.G.; Mbikay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A39180
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30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kallikrein.
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                 #domain signal sequence #status pr.
#product plasma kallikrein heavy c.
experimental #label MATI\
#domain apple repeat #label AP2\
#domain apple repeat #label AP3\
#domain apple repeat #label AP3\
#domain apple repeat #label AP4\
#domain apple repeat #label AP4\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translated from GB/EMBL/DDBJ
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light
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y chain #status
chain
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391-621
21-104-77,51-57,
111-194,137-166,
141-147,201-284,
227-256,231-237,
292-375,314-245,
322-328,340-245,
383-503,419-435,
                                                                     #authors McMullen, B.A.; Fujikawa, K.; Davie, E.W.
#journal Biochemistry (1991) 30:2050-2056
#title Location of the disulfide bonds in human plasma
prekallikrein: the presence of four novel apple
the amino-terminal portion of the molecule.
#cross-references MUD:91152016
                                  #accession A3793
##molecule_type
                                                                                                                                                                                                                                                                              #accession
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                                                                                                                                                                                                                                                                                             #cross-references MUID:86243359
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                                                                                                                                                                                                                                                                                                                                                                              authors
                                                                                                                                                                                                                                                                                                                                                        Journal
                                                                                                                                                                                                                                                                                                                                                                                              IONS
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#residues 1-638 ##label CHU
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                        ##residues
                                                                                                                                                                                                               ##cross-references GB:M13143; NID:g190262; PIDN:AAA60153.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLP 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACLPLWRERPQKTASNCYITGWGDT-GRAYSRT-LQQAAIPLLPKRFCEERYKG-RFTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAF 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICLP-SKADTNTIYTNCWVTGWGYTKERGETQNILQKATIPLVPNEECQKKYRDYVITKQ 560
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Similarity 38.9%;
95; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  816
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                                                                                                                                                                                                                                                                                                             Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Biochemistry (1986) 25:2410-2417 Human plasma prekallikrein, a zymogen to a that contains four tandem repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQHUP #type complete
plasma kallikrein (EC 3.4.21.34) precursor - human
kininogenin; plasma prekallikrein
#formal_name Homo sapiens #common_name man
13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change
                                                               A37939
                                                                                                                                                                                                                                                                              A00921
                                                                                                                                                                                                                                                                                                                                                                                                                 A00921; A37939
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                                                                                                                                                                                                                                                                                                                                                                                                                                     .8-Jun-1999
protein
20-27;40-46,'X',48,'H';50,'X',52-70,'H';75-76,'X',78-80;
103-113;131-140;141-143;'S',144-146;147-159;187-193,
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#active_site His, Asp,
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#molecular-weight 71273 #checksum 2
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Pred. No. 2.92e-109;
60; Mismatches 71;
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Best Local Similarity 39.6%;
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390-391
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141-147,201-284,
227-256,231-237,
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383-503,419-435,
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p_position 4q35-4q35
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232-248;254-255,'X',257-259,260-283,'X',285,287-291,
'X',233-295;314-317,'X',319-320;321-324,'Y',329-333;
334-339,'X',341-346,'X',348-350;351,'XXT',355;380-382,
'X',348-386,417-418,'X',420-434,'X',435-446,489-502,
'X',546-566;510-525;538-551;562,'X',564-567;573,'X',
'X',546-566;510-525;538-551;562,'X',564-567;573,'X',
'X',546-566;510-525;538-551;562,'X',564-567;573,'X',
'X',546-566;510-525;538-551;562,'X',564-567;573,'X',
'X',546-566;510-525;538-551;562,'X',564-567;573,'X',
'X',546-566;510-525;538-551;562,'X',564-567;573,'X',
'X',546-566;510-525;538-551;562,'X',564-567;573,'X',
'X',546-456;510-525;538-551;562,'X',564-567;573,'X',
'X',546-456;510-525;538-551;562,'X',586-562,'X',564-567;573,'X',
'X',546-456;510-525;538-551;562,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586,'X',586
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                                                                                                                                                                                                   PICLP-SKGDTSTIYTNCWVTGWGFSKEKGEIQNILQKVNIPLVTNEECQKRYQDYKITQ
RMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSA 811
                                                                   RMVCAGY-KEGGK-DACKGDSGGPLVCKHNG-MWRLVGITSWGEGCARREQPGVYTKVAE
                                                                                                                                      PACLPLWRERPQKTASNCYITGWG-DTGRA-YSRTLQQAAIPLLPKRFCEERYKG-RFTG
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                                                                                                                                                                                                                                                                                                                                  SG-ILNLSDITKDTPFSQ-I--KEIIIHQNYKVSEGNHDIALIKLQAPLN-YTEF--QK- 500
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blood coagulation; duplication; fibrinolysis; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #length 638
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/th 638 #molecular-weight 71369 #checksum 5
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#cleavage_Site Arg-Ile (coagulation factor XIIa) #status
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#domain apple repeat #label AP2\
#domain apple repeat #label AP3\
#domain apple repeat #label AP4\
#domain apple repeat #label AP4\
#domain plasma kallikrein light chain
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#product plasma kallikrein #status predicted #label MAT\
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Pred. No. 2.92e-109;
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#title
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title Molecular cloning of preproacrosin and analysis of its expression pattern in spermatogenesis. #cross-references MUID:89325301 #accession S04940
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##residues 'x',18,'x',20-25,'x',27-32,'X',34-38,'X',40-50
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##residues 1-415 ##label BAB
                                                                      ##cross-references EMBL:X14844; NID:g1867; PIDN:CAA32948.1; PID:g1868
##note the difference at the carboxyl end is due to a
                                                                                                                                                                                              ##molecule_type mRNA
##residues 1-7,
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Is spermingen a modified proacrosin? Isolation, purification, and partial characterization of low-molecular-mass boar proacrosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsaousidou, S.; Engel, W. Eur. J. Biochem. (1989) 182:563-568
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Activation and maturation mechanisms of boar acrosin zymogen based on the deduced primary structure.
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acrosin (EC 3.4.21.10) precursor - pig
53K fucose-binding protein
#formal_name Sus scrofa domestica #common_name domestic pig
10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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Acrosin shows zona and fucose binding, novel
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'GN',396,'LVE',399-409,'RRTARLLI' ##Label ADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                              the authors translated the codon CCT for residue 240 Ala, GCC for residue 264 as Gly, and ACC 
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                                                                                                                                            7,9-210,'Q',212-216,'VT',219-346,'A',348-388,390-398,'KELL' ##label AD2
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Best Local Similarity 39.1%;
Matches 99; Conservative
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71-87,175-244,
207-223,234-264
86,140,238
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300-374
19,208
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#journal FEBS Lett. (1999) 244:132-136
#title Activation of boar proacrosin is effected by processing both N- and C-terminal portions of the zymogen molecul #cross-references MUID:89171246
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#cross-references MUID:90306316
#accession S10695
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                                                                                                                                                                                                                                      634
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##residues 17-69 ##label
806
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##residues 40-62 ##label TO2
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                                     YTSTWPYLNWIAS
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YTKVSAFVPWIKS
                                                                                                               GRIRSTNVCAGYPRG-K-IDTCQGDSGGPLMCRDRAENTFVVVGITSWGVGCARAKRPGV 272
                                                                                                                                                      HVLPACLPLWRERPQKTASNCYITGWG----DTGRAYSRTLQQAAIPLLPKRFCEE-R-YK
                                                                                                                                                                                                                                                                           IFGANEVVWGSNKPVKPPLQERF-VEEIIIHEKYVSGLEINDIALIKI-TPPVPCGPF-- 155
                                                                            GRFTGRMLCAGNLHEHKRVDSCQGDSGGPLMC-ERPGESWVVYGVTSWGYGCGVKDSPGV
                                                                                                                                                                                           -IGPGCLPQFKAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLELCNSTRWYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S12968
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FEBS Lett. (1990) 265:51-54
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#active_site His, Asp, Ser #status predicted
#th 415 #molecular-weight 45387 #checksum 6
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#product acrosin #status experimental #label MAT\
#product acrosin light (A) chain #status experimental
#label LCH\
#product acrosin heavy (B) chain #status experimental
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818
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56; 1
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Pred. No. 1.65e-104;
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Best Local
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25-158
70-86
85,139,238
175-244
#authors Klemm, U.; Flake, A.; Engel, W.
#journal Biochim. Biophys. Acta (1991) 1090:270-272
#title Rat sperm acrosin: cDNA sequence, derived primary
and phylogenetic origin.
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234-264
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18,208
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                                                                                                                                                                                                                                                                                                                                                          273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 IVSGQSAHVGAWPWMVSLQIFTSHNSRRYHACGGSLLNSHWVLTAAHCFDNKKKVYDWRL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 29.6%;
Local Similarity 40.7%;
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A37344
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Willison, K.; Engel, W.
Differentiation (1990) 42:160-166
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acrosin (EC 3.4.21.10) precursor form 1 - mouse
#formal_name Mus musculus #common_name house mouse
19-Mar-1993 #sequence_revision 19-Mar-1993 #text_change
                                                                                                                                                          #formal_name Rattus norvegicus #common_name
31-Dec-1993 #sequence_revision 31-Dec-1993 #
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#disulfide_bonds #status predicted\
#active_site His, Asp, Ser #status predicted\
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Pred. No. 3.43e-101;
48; Mismatches 84;
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##molecule_type DNA; mRNA
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Local Similarity 40.9%;
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                                                                                                                                                                                                                                                                                        VGPGCLPHFKSGPPRIPHTCYVTGWGYIKDNAPRPSPVLMEARVDLIDLDLCNSTQWYNG
                                                                                                                                                TATWDYLDWIAS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
#formal
                    acrosin (EC
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glycoprotein; hydrolase; serine protei
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__name Oryctolagus (
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                    precursor
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Similarity 39.1%;
99; Conservet'
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Primary structure of mouse proacrosin deduced from the cDNA sequence and its gene expression during spermatogenesis.
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Y.; Arai, Y
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acrosin (EC 3.4.21.10) precursor form 3 - mouse
#formal_name Mus musculus #common_name house mouse
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
22-Jun-1999
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Biochim. Biophys. Acta (1994) 1219:215-218
Cloning and sequencing of cDNAs for rabbit
a novel preproacrosin-related cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe, K.; Baba,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JX0172; JX0138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #length 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-Jun-1999
                                                                                                                                                                                                                                                                                                                              1-436 ##label WAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #domain trypsin homology #label TRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-431 ##label RIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #molecular-weight 46422 #checksum
                                                                                                                                                                                                                                             S.; Baba, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 555; DB 2; L
Pred. No. 5.24e-100;
54; Mismatches 81;
     NID: g220322; PIDN: BAA00651.1;
                                                                                                                                                                                                                                                                                                     NID: g238706; PIDN: AAB20293.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kashiwabara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serine proteinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 431;
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                                                                                                                                                                                                                                             Watanabe,
                                                                                                                                                                                                                                                                                                                                                                                                                                     acrosin
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                                                                                                                                                                                                                                                                                                  PID: g238707
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                                                                                                                                                                                                                                                Yano,
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REFERENCE
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1-19
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74-90,178-247,
210-226,237-267
89,143,241
235
                                                                                                                                                                                                                                                                                                                           #authors
#journal
#title
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22,211
  #authors
                                                                                                                                                                                           #accession
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                                                                                                                                                                                                                    #cross-references
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                                                                           ##molecule_type DNA
##residues 1-559 ##label
##cross-references GB:M31197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634
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                                                                                                                                                               ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 VFGAQEIEYGRNKPVKEPQQERYVQKIVIHEKYNVVTEGNDIALLKI-TPPVTCGNF--- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 IVSGQSAQLGAWPWMVSLQIFTSHNSRRYHACGGSLLNSHWVLTAAHCFDNKKKVYDWRL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLPACLPLWRERPQKTASNCYITGWG-DTGRA-Y-SRTLQQAAIPLLPKRFCE--ERYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYAVRVGDYHTLVP-EEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKVSAFVPWIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATWDYLDWIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFTGRMLCAGNLHEHKRVDSCQGDSGGPLMC-ERPGESWVVYGVTSWGYGCGVKDSPGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVTSTNVCAGY-PEGK-IDTCQGDSGGPLMCRDNVDSPFVVVGITSWGVGCARAKRPGVY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGPCCLPHFKAGPPQIPHTCYVTGWGYIKEKAPRPSPVLMEARVDLIDLDLCNSTQWYNG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acrosin is an acrosomal protease that plays an important in the initial stages of fertilization by providing both a trypsin-like serine protease activity and a lectin-like carbohydrate-binding activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 28.9%;
Similarity 40.1%;
A31597
Ny, T.;
                                                                                                                                                                                                                                                                Feng, P.; Ohlsson, M.; Ny, T.
J. Biol. Chem. (1990) 265:2022-2027
The structure of the TATA-less rat tissue-type plasminogen
activator gene. Species-specific sequence divergences in
the promoter predict differences in regulation of gene
                                                                                                                                                                                        A35029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #type complete
t-plasminogen activator (EC 3.4.21.68) precursor - rat
#formal_name Rattus norvegicus #common_name Norway rat
10-sep-1999 #sequence_revision 10-sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                            A35029
                                                                                                                                                                                                                                                                                                                                                                                                                                  A35029; A31597
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                                                                                                                                                                                                                 expression.
s MUID:90130448
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#active_site His, Asp, Ser #status predicted\
#binding_site substrate (Asp) #status predicted
#th 436 #molecular-weight 48929 #checksum 7575
                                                                                                                                                               preliminary
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#binding_site carbohydrate (Asn) (covalent) #status
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#product acrosin light chain #status predicted #label
  Leonardsson,
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                                                       GB:J05226
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Pred. No. 4.08e-98;
                                                                              NID:g207429;
                                                                                                          FEN
  G.,
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  Hsueh,
                                                                              PIDN: AAA42261.1;
  A.J.W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38-68, 66-75, 83-94,
838-105, 107-116,
124-205, 145-187,
176-200, 213-294,
234-276, 265-289,
297-266, 265-286,
348-417, 442-516,
474-490, 506-534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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30-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal #title
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213-294
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#cross-references MUID:89170114
#accession A31597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355,404,510
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##cross references GB:M23697; NID:g530159; PIDN:AAA41812.1; PID:g530160
IFICATION #superfamily tissue plasminogen activator; EGF homology;
fibronectin type I repeat homology; kringle homology;
trypsin homology
                                                                                                                                                              819
                                                                                                                                                                                                                                            761
                                                                                                                                                                                                                                                                                    497
                                                                                                                                                                                                                                                                                                                          707
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                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PWQAAIFYKNKRSPGERFLCGGVLISSCWVLSAAHCFVERF--PPHHLKVVLGRTYR-VV 377
                                                                                                                                                            VTK 821
                                                                                                                                                                                                    NMK 558
                                                                                                                                                                                                                                                                 GGNQDVHDACQGDSGGPLVC-MIDKRMTLLGIISWGLGCGQKDVPGIYTKVTNYLNWIQD 555
                                                                                                                                                                                                                                                                                                                      KTASNCYITGWG--DTGRAY-SRTLQQAAIPLLPKRFC-EER-YKGRFTGRMLCAGNLH-
                                                                                                                                                                                                                                                                                                                                                                                                                               PGEEEQTFEIEKYIVHKEFDDDTYDNDIALLQLRSDSSQCAQESSSVGTACLPD-PDVQL 436
                                                                                                                                                                                                                                          -EHKRV-DSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKS
                                                                                                                                                                                                                                                                                                                                                                PDWTECELSGYGKHEASSPFFSDRLKEAHVRLYPSSRCTSQHLFNKTITSNMLCAGDTRT 496
                                                                                                                                                                                                                                                                                                                                                                                                        PEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQ 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHCF-KRYGNSTRSYAVRVG-DYHTLV 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.9%;
Similarity 38.3%;
93; Conservation
              $29599  #type fragment corosin (EC 3.4.21.10) precursor - guinea pig (fragment) #formal_name Cavia porcellus #common_name guinea pig 22-Nov-1993  #sequence_revision 10-Nov-1995  #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #length 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (1988) 7:671-677 Cloning and characterization of a cDNA for rat tissue-type
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22-Jun-1999
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pth 559 #molecular-weight 62903 #c
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#binding_site carbohydrate (Asn) (c
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#domain kringle homology #label KR2\
#product t-plasminogen activator chain
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Pred. No. 7.03e-98;
58; Mismatches 76;
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                                                                                                            ##molecule_type_DNA
#residues 1-431 ##label RIC
##cross-references GB:X02419; NID
##CIOSS-references GB:X02419; NID
                                                                                              ##note
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##cross-references EMBL:Z12153; NID:g49559; PIDN:CAA78137.1;
FFICATION #superfamily acrosin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274
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Similarity 39.1%;
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Nagamine, Y.; Pearson, D.; Grattan, M. Biochem. Biophys. Res. Commun. (1985) 132:563-569 Exon-intron boundary sliding in the generation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerton, G.L.; Hoff, H.B.; Baba, T. submitted to the EMBL Data Library, May 1992 The amino acid sequence of guinea pig proacr
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#length 421 #checksum 9563
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                                                                                                                                                                                                                                                                   Nucleic Acids Res. (1985) 13:2759-2771
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17-Dec-1982 #sequence_revision 04-Dec-1986
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Pred. No. 1.21e-97
46; Mismatches 8
                                                                                                                                 NID:g37601; PIDN:CAA26268.1; PID:e300604;
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##cross-references EMBL:x02760; NID:g35297; PIDN:CAA26535.1; PID:g35298 REFERENCE S65783
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#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:4727-4731

#title Identification and primary sequence of an unspliced human

#cross-references MUID:84272706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal Gene (1985) 36:183-188
#title Molecular cloning of cDNA coding
#cross-references MUID:86056954
#accession JT0102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #title Molecular cloning, sequencing, and expression coli of human preprourokinase cDNA.
#cross-references_MUID:85203359
                                                                                                                                                                                                                   #cross-references MUID:83055084
#accession A37562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Yoshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.
Takahashi, K.; Sawasaki, Y.; Hanada, K.
Biochim. Biophys. Acta (1996) 1293:83-89
Characterization of single chain urokinase-type plasminogen
activator with a novel amino-acid substitution in the
kringle structure.
#cross-references_MUID:96186279
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##residues 1-213,'T',215-431 ##label NAG2

##cross-references GB:K03226; NID:g340155; PIDN:AAC97138.1; PID:g340158;

GB:D00244; NID:g220138; PID:d1000623; PID:g220139
                                                                                                                                                                                                                                                                                                                                                                                                     ##status preliminary
##molecule_type mRNA
##residues 21-140,'L',142-213,'I',215-431 ##label YOS
##cross-references EMBL:D11143; NID:g1311467; PIDN:BAA01919.1;
PID:d1002396; PID:g1199928
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DNA (1985) 4:139-146
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                 Eur. J. Biochem. (1982) 125:251-257
Human low-molecular-weight urinary urokinase. Partial
Characterization and preliminary sequence data of t
                                                                 W.; Studer, R.O.
Eur. J. Biochem. (
                                                                                                                                                                                                                                                                                      Hoppe-Seyler's Z. Physiol. Chem. (1982) The primary structure of high molecular
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Blasi, F.
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polypeptide chains
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                                                                                                                 J.; Nick, H.; Rickli,
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                                                                                                                                                                                                                                                                                                                                         Flohe,
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                                                                                                                                                                                                                                                                                                                                                                                                       #authors Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.
Mazar, A.P.; Olejniczak, E.T.; Xu, R.X.; Pederson, T.M.;
Henkin, J.; Fesik, S.W.
#submission submitted to the Brookhaven Protein Data Bank, January 1994
#cross-references PDB:1URK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #authors Kentzer, E.J.; Buko, A.; Menon, G.; Sarin, V.K.
#journal Biochem. Biophys. Res. Commun. (1990) 171:401-406
#title Carbohydrate composition and presence of a fucose-protein
inkage in recombinant human pro-urokinase.
#cross-references_MUID:90365737
#gene
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##residues 21-34 ##label RAB
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##residues 158-410 ##label STE
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##residues 156-176;179-193,'T',195,'T',197-224 ##label SCH
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##residues 21-30,'X',32,'X',34-38,'X',40-43 ##label KEN
                                        This enzyme is found in urine in a high molecular mass form, consisting of A and B chains, and a low molecular mass form, consisting of Al and B chains.

Urokinase-type plasminogen activator proteolytically activates plasminogen, and the inactive single-chain form is proteolytically activated by plasmin (see PIR:PLHU).
                                                                                                                                                                                                                                                             Spraggon, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.; Stuart, D.I.; Jones, E.Y. submitted to the Brookhaven Protein Data Bank, July 1995
                                                                                                                                                                                    annotation; X-ray crystallography, 2.5 angstroms, residues 168\text{--}175;179\text{--}426
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Biochem. Biophys. Res. Commun. (1990) 173:1058-1064
An amino-terminal fragment of urokinase isolated fro
prostate cancer cell line (PC-3) is mitogenic for
                                                                                                                                                                                                                                                                                                                                                        annotation; conformation and disulfide bond assignments by (1)H-NMR, residues 26-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li, X.; Smith, R.A.G.; Dobson, C.M. Biochemistry (1992) 31:9562-9571 Sequential (1)H NMR assignments and secondary structure of the kringle domain from urokinase.
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#title
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##molecule_type mRNA
##residues 1-560 ##label CHO
##cross-references GB:S83182; NID
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Local Similarity 36.9%;
nes 93; Conservative
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                                                                                                                                                                                                                                                                  Choi-Miura, N.H.; Tobe, T.; Sumiya, J.; Naka Mazda, T.; Tomita, M.
J. Biochem (1996) 119:1157-1165
Purification and characterization of a novel
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JC4795
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plasma hyaluronan-binding protein precursor - human
hepatocyte growth factor activator-like protein; PHBP
serine proteinase (EC 3.4.21.-)
#formal_name Homo sapiens #common_name man
15-Oct_1995 #sequence_revision 16-Aug-1996 #text_change
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homology; kringle homology; trypsin homology
fibrinolysis; glycoprotein; heterodimer; hydrolase; kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteolytically activates plasminogen fibrinolysis
                                                                                                                                                                     hyaluronan-binding protein (PHBP) from human plasma: three EGF, a kringle and a serine protease domain, si to hepatocyte growth factor activator.
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#product urokinase-type plasminogen activator, single
chain form #status predicted #label MAT\
#product urokinase-type plasminogen activator chain A
#status experimental #label MPA\
#domain EGF homology #label EGF\
#domain EGF homology #label KRG\
#product urokinase-type plasminogen activator chain Al
#status experimental #label MPA\
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#status experimental #label MPB\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 545; DB 1;
Pred. No. 1.21e-97;
60; Mismatches 85
NID:g1836158; PIDN:AAB46909.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85; Indels
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ACCESSIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115-125,120-136,
138-147,154-165,
159-176,178-187,
194-276,215-257,
246-271,301-435,
347-363,355-424,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local
Matches
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                                   #journal #title
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154-187
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314-550
314-516
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505-533
                                                                                    #authors
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                                                                                                                                                                                                                                                                                                                                                                           765 VDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKSVTK 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 EE-IGVQQIVIHREY--RPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQKT 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            592 QVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAVRVGDYHTLVPEEFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 QSSLPLTISMPQGHF-CGGALIHPCWVLTAAHC-T--DIKTRHLKVVLGD-QDLKKEEFH 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##experimental_source plasma
##note parts of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##cross-references GDB:457396
                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                               -DTCQGDSGGPLTCEKDG-TYYVYGIVSWGLECG-K-RPGVYTQVTKFLNWIKATIK 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASNCYITGWG--DTGRAYSRTLDQAAIPLLPKRFCEER--YKGRFTGRMLCAGNLHEHKR 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSECHISGWGVTETGKG-SRQLLDAKVKLIANTLCNSRQLYDHMIDDSMICAGNLQKPGQ 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQSFRVEKIFKYSHYNERDEIPHNDIALLKLKPVDGHCALESKYVKTVCLP---DGSFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.6%;
Similarity 41.8%;
99; Conservation
Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T. J. Blochem. (1998) 124:784-789
A novel low-density lipoprotein receptor-related protein with type II membrane protein-like structure is abundant in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a disulfide-bonded heterodimer of chains produced same precursor; the catalytic chain is degraded chain lacking the active site serine residue #superfamily plasma hyaluronan-binding protein; EC kringle homology; trypsin homology chondroitin sulfate proteoglycan; glycoprotein; gr factor; hyaluronic acid; hydrolase; kringle; pla
                                                                                                                                                             JE0315 #type complete
low-density lipoprotein receptor-related protein - mouse
#formal_name Mus musculus #common_name house mouse
16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #length
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#active_site His, Asp, Ser #status predicted
#th 560 #molecular-weight 62671 #checksum 4
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#status predicted #label 50K\
#domain EGF homology #label EG1\
#domain EGF homology #label EG2\
#domain EGF homology #label EG3\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #product plasma hyaluronan-binding protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #binding_site carbohydrate (Asn) (covalent) #status
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#domain trypsin homology #label TRYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 541; DB 1; Length 560; Pred. No. 1.07e-96; 45; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
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##status preliminary
##molecule_type mRNA
##residues 1-1113 ##label TOM
##cross-references DDBJ:AB013874
CLASSIFICATION #superfamily trypsin homology
FEATURE #domain trypsin homology
869-1097 #length 1113 #molecular-weigh
Search completed: Mon Mar 13 10:18:43 2000 Job time: 20 secs.
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                                                                                                                                           1039 G--YESGTVDSCMGDSGGPLVCERPGGQWTLFGLTSWGSVCFSKVLGPGVYSNVSYFVGW 1096.
                                                                                                         1097 I 1097
                                                                                                                                                                                                                  816 I 816
                                                                                                                                                                                                                                                                                             638 RVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHYLPAC 697
                                                                                                                                                                                                                                                                                                                    924 VFGINNLDHPSGEMQTRFVKTILLHPRYSRAVVDYDISVVEL--SDDI-NE-TSYVRPVC 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heart.
JE0315
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US-09-147-947-6-04.rai

(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

dd_h protein - protein database search, using Smith-Waterman algorithm

Mon Mar 13 10:29:12 2000; MasPar time 4.72 Seconds 277.482 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: Title: >US-09-147-947-6 (227-327) from US09147947A.pep (4 of 6) 757

1 IRLAGGSSVHEGRVELYHAG.....KSSWGEHNCGHKEDAGVSCT 101

Scoring table: PAM 150 Gap 11

Searched:

131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: T:5K_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Mean 26.593; Variance 104.340; scale 0.255

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

٠,	Score	Query Match	Length	DB	ID	Description		Pred. No.
9	435	7.	453	4.	5510466-4	Patent No.	5510466.	1.34e-34
Ŋ	428	56.5	451	ω	-US9	ce 2,	Appli	6e-3
ω	428	9	451	N	0	Sequence 2,	ati	ū
4	428	6	451	ᆫ	S		licat	.26e-3
G	428	σ.	451	N	US-08-948-		licat	6e-3
σ	427	5	451	-	US-08-154-	æ	licat	.24e-3
7	412	٠.	585	ب	-47	Sequence 10	plica	.44e-3
ω	412	4	585	2	US-08-316-		lica	.44e-3
ဖ	412	4	585	Н	US-08-477-	Sequence 10	ద	.44e-3
 0	365	œ	1290	Ь		Sequence 2,	icat	.75e-2
 1	355	5	489	Ŋ	8-79	Sequence 7,	Applicatio	.00e-2
 12	355	46.9	518	ب	-39		Applicatio	0e-
 L ₃	338	4.	495	N	US-08-794-	Φ	Applicatio	.72e-2
 4	338		520	N	-80-	Sequence 6,	licat	.72e-2
 5	125	. 0	798	Н	US-08-200-	Sequence 2,	Applicatio	
 16	125		798	ω	PCT-US94-0	Ø	licat	.35e-0
 17	88	1	356	N	-80	Ø	Applicatio	٠,
 18	83	-	1167	ш	US-08-474-	Ø	licat	
 19	83	1	1167	N	8-8	O	Applicatio	
 20	83	-	1167	ш	8-17	O	Applicatio	1.09e+01
 21	83		1167	N	8-77	Φ	licat	
 22	83	!	1167	Н	US-08-100-	Φ	Applicatio	
 23	79	10.4	1168	1-1	8	Sequence 4,	licat	2.31e+01

SULT	44444000000000000000000000000000000000	24
H	77777777777777777777777777777777777777	79
	00000000000000000000	10.4
	1168 1130 1130 3111 3111 3111 323 233 425 1165 1165 1165 1176 1177 1177 1177	1168
	246661111111111111111	ω
ALIGNMENTS	544418-08-962- US-08-125- US-08-125- US-08-125- US-08-125- US-08-125- US-08-477- US-08-190- US-08-190- US-08-190-1 US-08-190-1 US-08-190-1 US-08-190-1 US-08-190-2 US-08-190-2 US-08-190-2 US-08-190-2 US-08-190-2 US-08-190-2 US-08-190-2 US-08-190-2 US-08-190-2 US-08-190-3	PCT-US95-1
	55. 82. 1114. 58.11.	Sequence 4, Applicatio
		2.31e+01

RESULT ID P XX AC x XX DT	Qy Qy	X B O	SOCOCOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
PCT-US96-08081-2 STANDARD; PRT; 451 AA. xxxxxx	227 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286 412 GPIWLNEVFCFPKESSIEECRIRQWGVRACSHDEDAGVTCT 452 11:	atch 57.5%; Score 435; DB 4; Length 453; cal Similarity 54.5%; Pred. No. 1.34e-34; Indels 0; Gar 55; Conservative 18; Mismatches 28; Indels 0; Gar	1-JAN-1900 1-JAN-1900 atent No. 5510466. atent No.

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Query Match
Best Local Similarity
Thes 54; Conserv
                                                                                                                                                     Sequence 2, Application US/08973145
                                                                                                                                                                                                      xxxxxx
                                                                                                                                                                                                                              US-08-973-145-2
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                  Sequence 2, Application US/08973145 Patent No. 5919636
                                                                                                                                                                                                                                                                                                                     287
                                                                                                                                                                                                                                                                                                410 GPIWLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTCT 450
                                                                                                                                                                                                                                                                                                                                            350 VRLVGGSGPHEGRVEILHSGQWGTICDDRWEVRVGQVVCRSLGYPGVQAVHKAAHFGQGT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Applications GENERAL INFORMATION:
                                                                    GENERAL INFORMATION:
APPLICANT: Lysko, Paul G.
APPLICANT: Elshourbagy, Nabil A.
APPLICANT: Brawner, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (610) 270-5090 INFORMATION FOR SEQ ID NO: 2:
                                  APPLICANT: Brawner, Mary E.
TITLE OF INVENTION: Attachment Enhanced
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/non-
FILING DATE:
CLASSIFFT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Jervis, Herbert H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Attachment Enhanced 293 Cells NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                          GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A. ZIP: 19406-5090
                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                  LE TYPE: protein
451 AA; 49762 MW; 1024670 CN;
SEE: SmithKline Beecham
: Mailcode - UW2220, 709
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                             STANDARD;
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Pred. No. 7.26e-34;
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             709 Swedeland Road
                      Corporate
                                                                                                                                                                                                                            451 AA.
                                                          293 Cells
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US-08-453-117-2
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                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKlin
ADDRESSEE: U.S.
                                                                                                                                                                                                                                                                                                                         APPLICANT: Elshourbagy, Nabil A.
APPLICANT: Brawner, Mary E.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: FILING DATE:
                                                                                                                                                 STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19406-5090
                                                                                                                                                                                                       STREET: Mailcode - UW2220, 709 Swedeland Road CITY: King of Prussia
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REGISTRATION NUMBER: P-4
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                                                                                                                                                                                                                                                                                                                                                                                  Paul G.
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                 US/08/453,117
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Pred. No. 7.26e-34;
20; Mismatches 27
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ATTORNEY/AGENT INFORMATION:

Jervis, Herbert H

CLASSIFICATION:

NAME:

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Patent No.
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REFERENCE/DOCKET NUMBER: SBC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEPAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC -DOS/MS-DOS
OFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: (
                                                                ATTORNEY/AGENT INFORMATION:
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                             APPLICANT: Brawner, Mary E.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
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larity 53.5%;
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Pred. No. 7.26e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                           TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 451 amino acid TYPE: amino acid ·
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
NAME: NAME: 31,284
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDITAL TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,365
                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
                                                                                                       REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Joiner, Keith A.
TITLE OF INVENTION: Method for Treating Gram-Positive
TITLE OF INVENTION: Septicemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
JENCE 451 AA; 49762 MW; 1024670 CN;
                             MOLECULE TYPE:
ANTI-SENSE: N
                   HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                 TYPE: amino acid
STRANDEDNESS: si
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CLASSIFICATION:
                                        TOPOLOGY:
                                                                                                                                                                                                                                                                       ZIP: 30309-4530
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Similarity 53.5%;
54; Conservation
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Kreiger, Monty
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Pred. No. 7.26e-34;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 VRLVGGSGPHEGRVEILHSGQWGTICDDNWEVRVGQVVCRSLGYPGVQAVHKAAHFGQGT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5736340 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,791
FILING DATE: 07-JUN-1995
                                                                                APPLICATION NUMBER: US/O
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: GOldman, Kenneth M
                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBLICATION INFORMATION:
AUTHORS: Ashkenas, et
JOURNAL: J. Lipid Res
VOLUME: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                 TELEPHONE: (510) 420-3152
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPIWLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTCT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAGES:
                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                        REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 2595.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELEVANT RESIDUES IN SEQ ID NO: 1
WCE 451 AA; 49841 MW; 1025052 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             10, Application US/08473791
o. 5736340
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                                                                            Goldman, Kenneth M
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1400 Fifty-Third Street
                        (510)
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Halenbeck, Robert F.
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                                                                                                                   US/07/961,404
                                                                                                                                         US/08/316,714
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Pred. No. 9.24e-34;
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT
                                                  TELEX: N/A INFORMATION FOR SEQ ID NO:
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Local Similarity 53.5%;
es 54; Conservation
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                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/O'
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth M.
                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,71
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 420-3152
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 585 AA; 65330 MW; 1874129
                             SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUMBER OF SEQUENCES:
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CITY: E
STATE:
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                                                                      TELEFAX:
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                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                     ZIP: 94608
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     STRANDEDNESS: single
                   TYPE: amino acid
                                                                                                              REGISTRATION NUMBER:
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                                                                     (510) 658-5470
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Pred. No. 3.44e-32;
Pred. Mismatches 28;
                                                                                                              34,174
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SEQUENCE

MOLECULE TYPE:

LE TYPE: protein 585 AA; 65330 MW; 1874129 CN;

Query Match 54.4%; Best Local Similarity 53.5%;

Matches

Conservative 19; Mismatches 28;

Score 412; DB 2; Pred. No. 3.44e-32;

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GENERAL INFORMATION:
APPLICANT: Koths, K
APPLICANT: Halenbec
                                               TELEX: N/A
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 585 amin Type:
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TOPOLOGY: li
MOLECULE TYPE:
QUENCE 585 AA;
                                                                                                                     REFERENCE/DOCKET NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 2595.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                     ZIP: 94608
COMPUTER READABLE FORM:
                                                                                                                                                              FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth M
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/477,674
FILING DATE: 07-UN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                  APPLICATION NUMBER: US/0:
FTLING DATE: 15-OCT-1992
                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1400 Firt
CITY: Emeryville
                                   STRANDEDNESS:
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                                              amino acid
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                                                       585 amino acids
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                                                                                                       (510) 658-5470
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                         linear
                                                                                                                    (510) 420-3152
  protein
65330 MW;
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   1874129
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   CN;
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                                                                                            Query Match 48.2%;
Best Local Similarity 52.4%;
Matches 54; Conservative
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Best Local Similarity 53.5%;
Matches 54; Conservative
                                                                                                                                                 SEQUENCE
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350 GSGSIVLDDVACTGHEAYLWSCSHRGWLSHNCGHHEDAGVICS 392
                                         227
                                                                 292 VRLVNGGDRCQGRVEILYQ-GSWGTVCDDSWDTKDANVVCRQL-VCGWALSAPGSAHFGQ 349
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                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1290 amino acids
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                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wolffe, Susan A
REGISTRATION NUMBER: 33,56
                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 1290 AA; 141879 MW; 9315616 CN;
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC DOS,MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,350B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Li, Xiao
APPLICANT: Snyder, Solomon H
TITLE OF INVENTION: Ebnerin:
TITLE OF INVENTION: Protein A
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION: 202-508-9100
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                                      IRLAGGSSVHEGRVE-LYHAGQWGTVCDDQWDDADAEVICRQLGLSG-IAKAWHQAYFGE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: LV-
                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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1001 G Street, N.W.
                                                                                                                                                                                                                                              202-508-9299
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                                                                                            Score 365; DB 1;
Pred. No. 2.75e-27
17; Mismatches 28
                                                                                                                                                                                                                                                                                                 33,568
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19; Mismatches 28; Indels
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Pred. No. 3.44e-32;
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                     US-08-392-367B-2
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                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
EILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gross, Mitchell APPLICANT: Lysko, Paul TITLE OF INVENTION: Human MITTLE OF INVENTION: eptor
                                                              GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 04-FEB-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                  LENGTH: 489 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                              TELEX:
                                                                                                                                                                                                                                                                                          TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                 NAME: Han, William T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                h 46.9%;
Similarity 50.5%;
51; Conservative
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5. 5916766
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489 AA; 49441 MW; 1141296 CN;
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                     STANDARD;
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                                                                                                                                                Score 355; DB 2; Le
Pred. No. 3.00e-26;
23; Mismatches 22;
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                    518 AA
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                                                                                          287
                                                                                                                                 227
                                                                                                                                            423 VRIMGGIN-R-GRAEVYYNNEWGTICDDDWDNNDATVFCRWLGYS-RGRA-LSSY-GGGS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2
Patent No.
                                                                                                             478 GNIWLDNVNCRGTENSLWDCSKNSWGNHNCVHNEDAGVECS 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5691197
TITLE OF INVENTION:
                                                                                                                                                                       Local Similarity hes 51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inc
MEDIUM TYPE: 720 kb storable
COMPUTER: IBM PS/2, Model 35 S)
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           TELEX: (216) 980162
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TETELECOMMUNICATION INFORMATION: TELEPHONE: (216) 861-5582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                        GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 Superior Avenue STREET: Suite 700 CITY: Cleveland
                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 44114-2518
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                                                                                                                                                                                                                                                      ENGTH:
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o. 5691197
                                                                                                                                                                                                               518 AA; 52730 MW; 1281000 CN;
                                                                                                                                                                                                                                         : 518 amino acids amino acid
                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                               : (216) 861-5582
(216) 241-1666
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                                                                                                                                                                                 50.5%;
                                                 STANDARD;
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Sequence 2, Application US/08794795

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t Local Similarity
                                                                                                                                                                                                                                                                                            SEQUENCE
                                          Sequence 6, Application US/08794795
         Sequence 6, Application US/08794795 Patent No. 5916766
                                                                                                                                                                             454 GQIWLDNVQCRGTESTLWSCTKNSWGHHDCSHEEDAGVECS 494
                                                                                                                                                                                                   227 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
                                                                                                                                                                                                                       399 VRIVGSSN-R-GRAEVYYSGTWGTICDDEWQNSDAIVFCRMLGYS-KGRALYKV--GAGT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08794795
                                                                                                                                                        287 GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,795
FILING DATE: 04-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ATG50009P
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 495 AA; 49764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lysko, P
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKline
STREET: 709 Swedeland
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Gross, Mitchell
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49764 MW; 1218428 CN;
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25; 1
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Pred. No. 1.72e-24;
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                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                  Sequence 2, Application US/08200900A
                                                                   Sequence 2, Application US/08200900A Patent No. 5665566
                                                                                                                                                                                                                  287
                                                                                                                                                                                                                                                                                   424 VRIVGSSN-R-GRAEVYYSGTWGTICDDEWQNSDAIVFCRMLGYS-KGRALYKV--GAGT 478
                                                                                                                                                                                                                                      479 GQIWLDNVQCRGTESTLWSCTKNSWGHHDCSHEEDAGVECS 519
                                                                                                                                                                                                                                                               227 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
                                            GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                     Match 44.68;
Local Similarity 46.58;
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 520 amino acid
          TITLE OF INVENTION: CI
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: ATG50009P
FILING DATE: 22-WAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 610-270-5219
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ADDRESSEE: SmithKline
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                                                                                                                                                                                                                  GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Han, William T REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 04-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      LE TYPE: peptide
520 AA; 52658 MW; 1340662 CN;
                                                                                                                                                                                                                                                                                                                                                                                                i: 520 amino acids amino acid
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Lysko, Paul
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 Genetics Institute,
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04-FEB-1997
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Inc.
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                                                                                                                                                                                  STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
FILING DATE: 23-FEB-1994
CLASSIFICATION ** 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEPHONE: (617) 876-1170 X8574
TELEPHONE: (617) 876-1170 X8574
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
C. LENGTH: 798 amino acids
C. TYPE: amino acids
C. TYPE: amino acids
C. TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 798 AA; 88937 MW; 3292434 CN;
                                                                                                                                                       Query Match 16.5%; Score 125; DB 1; Best Local Similarity 26.8%; Pred. No. 2.35e-03; Matches 22; Conservative 21; Mismatches 35
287 GP-VMLDEVRCTGNELS-IEQC 306
                                  515 GPYVNLNTAPNGSLILTPSQQC 536
                                                                                                 227 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
                                                                                                                                                         Mismatches 35;
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Search completed: Mon Mar 13 10:29:19 2000 Job time: 7 secs.

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Tabular output not generated. Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Mon Mar 13 10:28:17 2000; MasPar time 10.34 Seconds 460.695 Million cell updates/sec **************

(MT)

Description: Perfect Score: Title: >US-09-147-947-6 (227-327) from US09147947A.pep (4 of 6) 757

Sequence: 1 IRLAGGSSVHEGRVELYHAG.....KSSWGEHNCGHKEDAGVSCT 101

Scoring table: PAM 150 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: pir62
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 37.625; Variance 64.653; scale 0.582

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score	704	444	436	430	428	428	427	416	416	416	416	412	401	397	384	381	373	365	355	325	321	293	158	
Query	ω	58.7	7.	5	9	9	9	5	5		Š	4.	ω	.2	0	0	9	8	6		2	ω.	20.9	
Length	761	453	454	458	451	454	2153	1116	1149	1151	1156	585	504	918	577	600	1436	1290	518	468	626	532	1034	
₽B		N																						
ID	575	S08276	686	44	A38415	A44407	T14893	S36077	138006	I38004	I38005	A47161	S56745	JC4361	A53202	S56744	A46496	19	584	674	910	N	99	
Description	brain-specific serine	ceptor I,	cave			ຜ	re	0 antigen - huma	gen (e	0 antigen (c	0 antigen (Mac-2-binding glycopr	GM31-1	Ω.	in C-associ	clone pGM7-1	en WC1.1	precur	macrophage bacteria-b	T-cell glycoprotein C	mscd6 precursor - mou	ct receptor p	eptidase (
Pred. No.		-77	. 66	.15e-7	.33e-7	- 7	.68e-7	.99e-7	.99e-7	.99e-7	.99e-7	.67e-6	.73e-6	7e-6	თ	.24e-6	e-6	.02e-5	.92e-5	.17e-4	.29e-4	.67e-4	.17e-1	

11.0 1680 2 A43434	11.0 494 2 T05302	3 84 11.1 2825 2 T14271 Doc4 protein,	2 84 11.1 741 2 A47063 cellulase SS	1 84 11.1 558 2 T15448 hypothetical	0 84 11.1 76 2 I39960 hypothetical	9 85 11.2 768 2 S76977 p	.4 1113 2 JE0315	7 86 11.4 810 2 S67050	6 87 11.5 226 2 D69156 '	5 90 11.9 527 2 B70920	4 91 12.0 603 2 S76615	3 95 12.5 425 2 B64316	2 99 13.1 494 1 A29079	1 101 13.3 501 1 S43536 T	0 103 13.6 403 2 T02513 hypoti	9 104 13.7 613 2 S15468 compl	8 112 14.8 495 1 A26396 T-cel	7 115 15.2 442 2 I47074 gene CD5	6 125 16.5 1035	5 126 16.6 1019 1 A56318 enteropeptidase	4 127 16.8 495 1: S11270 T-cell surface	use hit. No. 2
furin (EC 3.4.21.75)	vacuolar processing e	protein,	lulase SS		prot	pleD-4 protein - Syne	low-density lipoprote	probable membrane pro	conserved hypothetica	hypothetical protein	hypothetical protein	restriction modificat	lymphocyte surface gl	T-cell surface glycop	hypothetical protein	complement C3b/C4b in	T-cell surface glycop	protein	enteropeptidase (EC 3	enteropeptidase (EC 3		
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ALIGNMENTS

Db 226 GPILLDEVRO	Db 166 IRLVGGNSGH - Qy 227 IRLAGGSSVI	Query Match Best Local Similar Matches 90; co	562,612,711 #le	513-516 517-755 93,521,569	166-266,273-372, 386-486	85-157 163-266	KEYWORDS gl: FEATURE	##experimenta CLASSIFICATION #S	##molecule_type mRNA ##residues 1-76 ##cross-references D	c; #cross-references #accession JC5	#journal Bio #title Mo.	ACCESSIONS JC REFERENCE JC #authors Yan	RESULT 1 FITTLE br. ORGANISM #f. DATE 24
GPILLDEVRCTGNEMSIEQCPKSSWGEHNCGHKEDAGVSC 265	IRLVGGNSGHEGRVELYHAGQWGTICDDQWDNADADVICRQLGLSGIAKAWHQAHFGEGS 225 :	h 93.0%; Score 704; DB 2; Length 761; Similarity 90.0%; Pred. No. 1.86e-138; 90; Conservative 7; Mismatches 3; Indels 0; Gaps 0;	predicted\ #active_site His, Asp, Ser #status predicted #length 761 #molecular-weight 84136 #checksum 5449	<pre>#domain furin binding #status predicted #label FRB\ #domain trypsin homology #label TRY\ #binding_site carbohydrate (Asn) (covalent) #status</pre>	#domain scavenger receptor cysteine-rich #status predicted #label SRC\	<pre>#domain kringle-like #status predicted #label KRI\ #domain scavenger receptor cysteine-rich domain homology #label SRC7\</pre>	glycoprotein; hydrolase; serine proteinase	##experimental_source brain FICATION #superfamily trypsin homology; scavenger receptor Cvsteine-rich domain homology	##molecule_type mRNA ##restiques 1.701 ##label YAM ##ross-references DDBJ.D89871	cysteine-rich motifs. ces MUID:98008848 JC5759	Biochem. Biophys. Res. Commun. (1997) 239:386-392 Molecular cloning of a novel brain-specific serine protease with a kringle-like structure and three scavenger receptor	JC5759 JC5759 JC5789 JC5789 JC5789 JC5759 JC5759 JC5759 JC5759	<pre>JC5759 #type complete brain-specific serine proteinase (EC 3.4.21) - mouse #formal_name Mus musculus #common_name house mouse 24 Jan-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999</pre>

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GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSC 326

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##residues 1-454 ##label BIC
##cross-references GB:L11693; NID:g165508; PIDN:AAA31402.1; PID:g165509
##CICATION #superfamily unassigned collagens; scavenger receptor
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J. Clin. Invest. (1992) 90:1450-1457
Rabbit aortic smooth muscle cells express
macrophage scavenger receptor messenger
from endothelial cells.
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#formal_name Oryctolagus cuniculus #common_name
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*accession 156374
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#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8810-8814

An ancient, highly conserved family of cysteine-rich protein domains revealed by cloning type I and type II murine macrophage scavenger receptors.

#cross-references_MUID:91062370
  354-457
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                                                                    ##residues 5-458 ##label RES
##cross-references GB:L04274; NID:g293745; PIDN:AAA39747.1;
FICATION #superfamily unassigned collagens; scavenger reco
                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status preliminary
##molecule_type mRNA
##residues 349-458 ##label FRE
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##residues 1-458 ##label DOI
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macrophage scavenger receptor type I
#formal_name Mus musculus #common_name house mouse
30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
20-Sep-1999
                                                                                                                                                                                                                                                         J. Lipid Res. (1993) 34:983-1000
Structures and high and low affinity ligand binding
properties of murine type I and type II macrophage
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Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger
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                                              cysteine-rich domain
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#domain scavenger receptor cysteine-rich domain homology
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                                                                      scavenger receptor
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#accession A44408
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##molecule_type nucleic acid

##residues 155-272 ##label EMI

##note sequence extracted from NCBI backbone (NCBIP:123189)
410 GPIWLNEVFCFGRESSIEECKIROWGTRACSHSEDAGVTCT 450
                                                                                                                                                                                                                                                                                                                ##cross-references G
#p_position 8p22-8p22
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##residues 1-451 ##label MAT
##cross-references GB:D90187; NID
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                                                   IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y.; Wada, Y.; Kanamori, H.; Yazaki, Y.; Takahashi, E.;
Lepert, M.; Lalouel, J.; Kodama, T.; Mukai, T.
J. Biol. Chem. (1993) 268:2120-2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suzuki, H.; Kobari, Y.; Miyai, T.; Takahashi, K.; Cohen, E.H.; Wydro, R.; Housman, D.E.; Kodama, T. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9133-9137
Human macrophage scavenger receptors; primary structure,
                                                                                                                                                                                                                                                            alternative splicing;
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Emi, M.; Asaoka, H.; Matsumoto,
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                                                                                                                                                                                          #length 451
                                                                                                                                                                                                                                                                                            #superfamily unassigned collagens; scavenger
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Pred. No. 3.33e-73;
20; Mismatches 27;
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Pred. No. 1.15e-73;
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Similarity 53.5%;
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##status preliminary; translated
##molecule_type mRNA
##residues 1-2153 ##label PAN
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##molecule_type nucleic acid
##residues 1-454 ##label DOI
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                                                                                                                                                                                                                                                                     Origins of immunity: transcription factors and homologs of effector genes of the vertebrate immune system expressed sea urchin coelomocytes.
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Nakamura, H.; Vesugi, S.; Imanishi, T.;
Itakura, H.; Yazaki, Y.; Matsumoto, A.;
J. Biol. Chem. (1993) 268:2126-2133
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cysteine-rich domain |
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                                                                                                                                                                                                                                                                                                                                           Pancer, Z.; Rast, J.P.; Davidson, E.H. Immunogenetics (1999) 49:773-786
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                                            #molecular-weight 226556
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#journal Eur. J. Immunnol. (1993) 23:2320-2325

#title A new macrophage differentiation antigen which is the scavenger receptor superfamily.

#cross-references_MUID:93380506
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##cross-references EMBL:Z22968; NID:g312141; PID:g312142
FICATION #superfamily scavenger receptor cysteine-rich domain homology
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     I38006 #type complete
MI30 antigen (extracellular variant) - human
#formal_name Homo sapiens #common_name man
17-May-1996 #sequence_revision 17-May-1996 #text_change
02-Aug-1996
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Db 1017 GPYMLNEVCKGNESSLWPCPARRWGHSPCGHEEDAAVNCT 1057 : : : : : Qy 287 GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327 RESULT 10 I38004 #type complete TITLE	0	#label SRC7\ #domain scavenger receptor cysteine-rich domain homc #label SRC8\ 954-1057 #domain scavenger receptor cysteine-rich domain homc 954-1057 #domain scavenger receptor cysteine-rich domain homc #label SRC9 #label SRC9 #label SRC9 #label SRC9	01 01 01	#label SRC3\ #label SRC3\ #label SRC4\ #label SRC4\ #label SRC4\ #label SRC4\ #label SRC4\ #label SRC3\ #label SRC4\ #label SRC4\	RENCE 138003 authors Law, S.K.; Micklem, K.J.; Shaw, J.M.; Zhang, X.P.; Do Willis, A.C.; Mason, D.Y. yournal Eur. J. Immunol. (1993) 23:2220-2325 title the scavenger receptor superfamily. cross-references MUID:93380506 accession 138006 ##status preliminary; translated from GB/EMBL/DDBJ ##nolecule_type mRNA ##residues 1.1149 ##label RES ##cross-references EMBL:222971; NID:g312147; PID:g312148 SIFICATION #superfamily scavenger receptor cysteine-rich domain #label SRC1\ ##label SRC1\ ##label SRC1\
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#label SRC2\

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##Cross-references EMBL.222970; NID:g312145; PID:g312146
IFICATION #superfamily scavencer reconstructions
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Eur. J. Immunol. (1993) 23:2320-2325

A new macrophage differentiation antigen which
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17-May-1996 #sequence_revision 17-May-1996
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Score 416; DB 2;
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#title
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#journal Biochem. Biophys. Res. Commun. (1
#title ligands for galectin-3.
#cross-references MUID:94296411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein, a new member of the superfamily defined by macrophage scavenger receptor cysteine-rich domain. #cross-references_MUID:93300818
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#*residues 1-585 ##label ULL
##cross-references GB:X79089; NID:g483473; PIDN:CAA55699.1; PID:g483474
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                                                                                                        ##note
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##residues 19-26 ##label IN2
                                                                                                                                                                                        ##molecule_type protein
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##cross-references GB:L13210; NID:g307152; PID:g307153
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Rosenberg, I.; Cherayil, B.J.; Isselbacher, K.J.; Pillai, S. J. Biol. Chem. (1991) 266:18731-18736
Mac-2-binding glycoproteins. Putative ligands for a cytosolic beta-galactoside lectin.
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C.; Tinari, N.; Rubistein, M.; Schlessinger, J.
FEBS Lett. (1993) 319:59-65
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Koths, K.; Taylor, E.; Halenbeck, R.; Casipit, C.; wan J. Biol. Chem. (1993) 268:14245-14249
Cloning and characterization of a human Mac-2-binding Cloning and characterization of the superfamily defined by
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J. Biol. Chem. (1994) 269:1840
The secreted tumor-associated
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Mac-2-binding glycoprotein precursor
90K tumor-associated protein precursor
#formal_name H0mo sapiens #common_name
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#title Bovine gall-bladder mucin contains two distinct tandem repeating sequences: evidence for scavenger receptor cysteine-rich repeats.
#cross-references MUID:95374471
#accession $56745
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Best Local
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19-22,'G','24-27,'XX',30 ##label ROS

##residues 19-22,'G','24-27,'XX',30 ##label ROS

##note the reported molecular weight of this protein,

designated Mac-2-binding glycoprotein 2 (M2BP-2), was

70K; the amino-terminal sequence of a related form of

98K, designated M2BP-1, could not be determined

FICATION #superfamily scavenger receptor cysteine-rich domain homology
                                                                                                                               297 TGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                                                                                                                                                                       328 GRVEIYHGGQWGTVCDDNWDVQDAQVVCRQLG-CGYAVSAPGNAYFGSGSGPITLDDVVC 386
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                                                                                                                                                                                                                                                                    Local Similarity 60.4%; tes 55; Conservation
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  cysteine-rich domain homology
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 #formal_name Petromyzon marinus #common_name
                    scavenger receptor Cys-rich
- sea lamprev
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#domain scavenger receptor cysteine-rich domain homology
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Pred. No. 5.73e-67;
13; Mismatches 21;
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Pred. No. 1.67e-69;
19; Mismatches 28
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896-918
40,545,575,
                                                                                                         #authors Chicheportiche, Y.; Vassalli, P.
#journal J. Biol. Chem. (1994) 269:5512-5517
#title Cloning and expression of a mouse macrophage cDNA coding
a membrane glycoprotein of the scavenger receptor
cysteine-rich domain family.
#cross-references_MUID:94164889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-918 ##label MAY
##cross-references GB:U20652; NID:g790233; PID:g790234
This protein is rich in cysteine and plays a role in intercellular
contacts and cell activation or differentiation in the cyclostom
##residues 1-577 ##label CHI
##cross-references EMBL:X67809; NID:g297032; PID:g297033; GB:X67803
##note sequence appears consistent with either a GPI anchor or
                                                                   ##molecule_type mRNA
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Matches 51; Conservative
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#journal Proc. Natl. Acad. Sci. U.S.A. (1993) 90:6815-6819
#title Cloning and characterization of cyclophilin C-associated protein: a candidate natural cellular ligand for cyclophilin C.
#cross-references MUID:93342080
#accession A48331.
                                                                                                                                                        ##molecule_type mRNA
1-24_','G',26-227,'P',229-465,'NE',468-572,'LH' ##label
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dd_u protein - protein database search, using Smith-Waterman algorithm

Mon Mar 13 10:27:15 2000; MasPar time 6.46 Seconds 466.945 Million cell updates/sec

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Description:
Perfect Score:
Sequence: 1 IRLAGGSSVHEGRVELYHAG.....KSSWGEHNCGHKEDAGVSCT 101 >US-09-147-947-6 (227-327) from US09147947A.pep (4 of 6) 757

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38

Statistics: Mean 38.669; Variance 61.361; scale 0.630

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1.6 591 1 LACI_CRYPA LACCASE PRECURSOR (EC 1.6 6845 1 EF2_CHLKE ELLONGATION FACTOR 2 (E 1.6 7712 1 LMA_DROME LAMININ ALPHA CHAIN PR 1.3 599 1 FRDA_HAEIN FUMARATE REDUCTASE FLA 2.3 707 1 GLH1_CAEEL ATP-DEPENDENT RNA HELI 3.4 707 1 LMA2_HUMAN LAMININ ALPHA-2 CHAIN 9 4.0 1 ATSB_KLEAE PUTATIVE ARYLSULFATASE 5.0 425 1 RB48_HUMAN CHROMATIN ASSEMBLY FAC 4.25 1 RB46_HUMAN HISTONE ACETYLTRANSFER 5.0 425 1 RB46_MOUSE HISTONE ACETYLTRANSFER 5.0 425 1 RB48_MOUSE HISTONE ACETYLTRANSFER 5.0 425 1 RB48_MOUSE HISTONE ACETYLTRANSFER 5.0 425 1 RB48_MOUSE HISTONE ACETYLTRANSFER 5.0 616 1 MS2_ARATH MALE STERILITY PROTEIN 5.0 632 1 YA28_SCHPO HYPOTHETICAL 71.9 %D P 5.0 638 1 KAL_MOUSE PLASMA KALLIKREIN PREC 5.0 1.165 1 CRYS_BACTA 1.32 KD CRYSTAL PROTEIN 5.0 1176 1 CRYS_BACTA 1.35 KD CRYSTAL PROTEIN 5.0 1176 1 CRYS	4.4 5	43	42	41	40	39	38	37	36	ω G	34	ω ω	32	31	30	29	28	27	26	25	24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMAGUCHI N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280
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                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                ACTION MAY SUBSERVE STRUCTURAL LEARNING AND MEMORY OPERATIONS. TISSUE SPECIFICITY: MOST ABUNDA
                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 3
                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: PLAYS A ROLE IN NEURONAL ACTION MAY SUBSERVE STRUCTURAL REOF LEARNING AND MEMORY OPERATIONS.
                                                                                                                                                                                                                                                                                             TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                          AND AMYGDALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9:207-219(1997).
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SRCR DOM
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annotation update)
3.4.21.-) (MOTOPSIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSURUOKA N., NAKAZATO H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECR 4.

SERINE PROTEASE.

ZYMOGEN ACTIVATION REGION.
REACTIVE BOND (POTENTIAL).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
POTENTIAL.
POTENTIAL.
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67D5272B
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DOMAINS.
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No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REORGANIZATIONS
                                                                                                                                                                                                                                                                                                                      FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   761
                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLASTICITY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Le
2.71e-163;
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                                                                                                                                                                                                                                                                                                                                                                                                CEREBRAL
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                                                                                                                            restrictions
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                                                                          and
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Best Local
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P21758;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last seque
01-FEB-1994 (Rel. 28, Last annot
MACROPHAGE SCAVENGER RECEPTOR TY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y13192; CAA73646.1; EMBL; D89871; BAA23986.1; MGD; MGI:1100881; PRSS12. PFAM; PF000530; SRCR; 3. PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
SEQUENCE
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ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                 MEDLINE;
KODAMA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
DISULFID
  "Coiled-coil fibrous domains mediate ligand binding by macrophage scavenger receptor type II.";
Nature 343:570-572(1990)
-i- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN AFTERIAL MALLS DURING ATHEROGENESIS.
TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING
                                                                                                                                                                            FISSUE=LUNG
                                                                                                                                                                                                                                    collagen-like coiled coils.";
Nature 343;531-535(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDL RECEPTOR I AND II).
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PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS00420; SPERACT_RECEPTOR;
                                                                                                                                        ROHRER L.,
                                                                                                                                                          MEDLINE; 90136973
                                                                                                                                                                                              SEQUENCE FROM N.A. (SHORT
                                                                                                                                                                                                                                                                           "Type I macrophage
                                                                                                                                                                                                                                                                                               KRIEGER
                                                                                                                                                                                                                                                                                                                                                                                                               Bovinae;
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                       SSUE=LUNG
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                                                                                                                                                                                                                                                                                                                 ., FREEMAN
                                                                                                                                                                                                                                                                                                                                   90136965
                                                                                                                                                                                                                                                                                                                                                                                                               Bos.
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                                                                                                                                        FREEMAN M.,
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91.0%;
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                                                                                                                                        KODAMA
                                                                                                                                                                                                                                                                                                                 ROHRER
                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE
                                                                                                                                                                                              FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
POTENTIAL.
POTENTIAL.
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Pred. No. 1
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                                                                                                                , PENMAN M.,
iate ligand b
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                                                                                                                                                                                                                                                                                                                 ZABRECKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pecora;
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L.46e-150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC32;
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                                                                                                                , KRIEGER M.;
binding by m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MACROPHAGE ACETYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265
                                                                                                                                                                                                                                                                                                                 MATSUDAIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovoidea;
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                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                            MSRE_RABIT STANDARD; PRT; 454 AA (05585; 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update) 01-0CT-1996 (Rel. 34, Last annotation update) MACROPHAGE SCAVENCER RECEPTOR TYPES I AND I
                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
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DOMAIN
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use by non-profit institutions as content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb
or send an email to license@isb-sib.ch).
                                                                                                            MSR1
  scavenger
                          BICKEL
                                       MEDLINE;
                                                 SEQUENCE FROM N.
                                                                         Eutheria;
                                                                                   Eukaryota;
                                                                                                 Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S08276; S08276. PIR; S08278; S08278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heptad repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00420; SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Endocytosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM;
                                                                                                                                                                                                                                              287
                                                                                                                                                                                                                                                                      412
                                                                                                                                                                                                                                                                                            227
                                                                                                                                                                                                                                                                                                                 352 VRLVGGSGPHEGRVEIFHEGQWGTVCDDRWELRGGLVVCRSLGYKGVQSVHKRAYFGKGT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MODIFIED LOW DENSITY LIPOPROTE SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II ALTERNATIVE PRODUCTS: THE TWO RECEPTOR (TYPES I AND II) ARE
                                                                                                                       RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF THE SAME GENE.
                                                                                                                                                                                                                                             GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT
                                                                                                                                                                                                                                                                GPIWLNEVFCFGKESSIEECRIRQWGVRACSHDEDAGVTCT 452
                                                                                                                                                                                                                                                                                     TRLAGGSSVHEGRVELYHAGOWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00530; SRCR; 1.
PF01391; Collagen; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X51689; CAA35987.1;
X54183; CAA38108.1;
. P.E., FREEMAN M.W.;
t aortic smooth muscle
ger receptor messenger
                                93016877.
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                         Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                        350
453
                                                                                    Metazoa;
                                                                                   cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                      I AND
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOW DENSITY LIPOPROTEINS (LDL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pattern;
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                                                                                                                       II).
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453
1108
271
343
343
453
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453
1142
1142
1142
1183
2266
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50056
                                                                                                                                                                                                                                                                                                                                                       58.7%;
55.4%;
                                                                         Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
                                                                                                                                                                                                                                                                                                                                                                                            MW.
                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.

POTENTIAL.

POTENTIAL.

OS -> PG (IN ISOFORM II).

MISSING (IN ISOFORM II).

MISSING (IN GROUPM II).
                                                                                                                                                                                                                                                                                                                                         Score 444; DB 1;
Pred. No. 4.98e-83;
18; Mismatches 27
 cells express inducible macrophage RNA that is absent from endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OT: Alternative splicing.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPHA-HELICAL COILED-COIL. COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYS-RICH
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                                                                         Oryctolagus
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FORMS OF MACROPHI
PRODUCED BY ALTEI
                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MACROPHAGE SCAVENGER
BY ALTERNATIVE SPLICING
                                                                                                                                   (MACROPHAGE ACETYLATED
                                                                                                                                                                                                                                              327
                                                                                                                                                                                                                                                                                                                                                                 Length 453;
                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
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Matches 5
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J. Clin. Invest.
                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
VARSPLIC
VARSPLIC
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBL; DATE PROMITE: PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger receptors.";
J. Biol. Chem. 268:2126-2133(1993).
-i- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL MALLS DURING ATHEROGENESS TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE TENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING MODIFIED LOW DENSITY LIPOPROTEINS (LDL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L11693; AAA31402.1; -.
EMBL; L11692; AAA31403.1; -.
EMBL; D13381; BAA02649.1; -.
PROSITE; PS00420; SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 93131972.
                                                                                                                                                                                                                                                                      SEQUENCE
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ITAKURA H., YAZAKI Y., MATSUMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                           413
                                                                                                                                 353 VRLVGGRGPHEGRVEILHNGQWGTVCDDHWELRAGQVVCRSLGYRGVKSVHKKAYFGQGT 412
  287
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SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
RECEPTOR (TYPES I AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF THE SAME GENE.
                       GPIWLNEVPCLGMESSIEECKIRQWGVRVCSHGEDAGVTCT 453
GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT
                                                                                       IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS
                                                                                                                                                                            similarity
55; Conser
                                                                                                                                                                                                                                                                      454
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                      A,
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                                                                                                                                                                                                                                                                                         54.5%;
                                                                                                                                                                                                                                                                    49745
                                                                                                                                                                                                                                                                      WW.
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THE TWO FORMS OF MACROPHAGE SCAVENGER
II) ARE PRODUCED BY ALTERNATIVE SPLIC
                                                                                                                                                                        Score 436;
Pred. No. 5.
17; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIGASHI K.I., KURIHARA Y.
ESUGI S., IMANISHI T., KAW
UMOTO A.;
                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
TPSATVR ->
MISSING (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocytosis; Coiled coil; tor; Alternative splicing. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA-HELICAL COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPACER (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                  ISSING (IN ISOFORM -> D (IN REF. 2). 5D780348 CRC32;
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                   DB 1;
.04e-81;
                                                                                                                                                                                                                                                                                                                                  RPVQLTP (IN ISOFORM II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COILED-COIL
                                                                                                                                                                            29;
327
                                                                                                                                                                                                                    Length 454
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KAWABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E PATHOLOGIC
G ATHEROGENESIS.
TORS MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲.
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RESULT ID M

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CCCCRRTTAAXRAR RRAKKAAA
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DOI T., WADA Y., KODAMA T., HIGASHI K.I. MIYAZAKI T., NAKAMURA H., UESUGI S., IM. A. ITAKURA H., YAZAKI Y., MATSUMOTO A.:
          EMBL; L04274; AAA39747.1; A
EMBL; L04275; AAA39748.1; A
EMBL; D13382; BAA02650.1; -
EMBL; M59445; AAA37464.1; -
EMBL; M59446; AAA37465.1; -
EMBL; U13873; AAC13774.1; -
PIR; A38260; A38260
MGD; MG1:98257; SCVR.
PROSITE; PS00420; SPERACT_R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P30204;
01-APR-1993
01-OCT-1996
15-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II
LDL RECEPTOR I AND II).
                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structures and high and low affinity murine type I and type II macrophage strain Res. 34:983-1000(1993).
                                                                                                                                                  modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                     evaluation of sequences that regulate cell line, P388D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 95395388.
AFTRING R.P., FREEMAN M.W.;
"Structure of the murine macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FREEMAN M., ASHKENAS J., REES D.J., JENKINS N.A., KRIEGER M.; "An ancient, highly conserved family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE OF 349-458 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Charged collagen structure mediates charged macromolecules by macrophage J. Biol. Chem. 268:2126-2133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSR1 OR SCVR.
 PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-4 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               revealed by cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASHKENAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRIEGER M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                              <del>----</del>
                                                                                                                                                                                                                                                                                                                                               Lipid Res. 36:1305-1314(1995).

- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC
- DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS.
TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE
ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING
                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
                                                                                                                                                                                                                                                              SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THE TWO FORMS OF MACROPHA
RECEPTOR (TYPES I AND II) ARE PRODUCED BY ALTEE
OF THE SAME GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                    MODIFIED LOW DENSITY LIPOPROTEINS (LDL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E FROM N.A.
: 93359822.
: J., PENMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PENMAN
                                                                               AAA39747.1; ALT_INIT.
AAA39748.1; ALT_INIT.
BAA02650.1; -.
AAA37464.1; -.
SRCR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sci. U.S.
           SPERACT_RECEPTOR;
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Sciurognathi; Muridae;
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scavenger receptors.";
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                                                                                                                                                                                                                                                                              MACROPHAGE SCAVENGER
BY ALTERNATIVE SPLICING
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P21757; P21759;
01-MAY-991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
"""" POPHAGE SCAVENGER RECEPTOR TYPES I AND II
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                                                                                                                                                    "Human macrophage scavenger receptors: primary structure, expression, and localization in atherosclerotic lesions."

Proc. Natl. Acad. Sci. U.S.A. 87:9133-9137(1990).

-!- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS.

TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC VARSPLIC
                               between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                        This
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HAYAKAWA I., KANAMORI H.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A MEDLINE; 91067661
                                                                                                                                                                                                                                                                                                                         Eutheria;
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Transmembrane;
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HOUSMAN D.E., KODAMA T.;
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                               RECEPTOR
OF THE SA
                                                                                         SUBCELLULAR LOCATION: TYPE II ALTERNATIVE PRODUCTS: THE TWO RECEPTOR (TYPES I AND II) ARE
                                                                                                                              MODIFIED LOW DENSITY LIPOPROTEINS SUBUNIT: HOMOTRIMER.
                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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., ABURATANI
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19; Mismatches
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Pred. No. 1
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ALPHA-HELICAL COILED-COIL
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H., TAKAKU
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F., SUZUKI I
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01-APR-1993 (Rel. 2
01-APR-1993 (Rel. 2
01-FEB-1994 (Rel. 2
ANTIGEN WC1.1.
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SEQUENCE
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                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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DOMAIN
                                                                                         "Molecular characterization of the WC1 antigen on bovine CD4-CD8-gamma delta T lymphocytes."; J. Immunol. 149:3273-3277(1992).
                                                                                                                                                                                                          Bos taurus (Bovine):
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                   WC11_BOVIN
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                        CLEVERS H.C.
                                                                                                                                  WIJNGAARD P.L.J., METZELAAR M.J., MACHUGH N.D.,
                                                                                                                                              MEDLINE; 93056489
                                                                                                                                                         TISSUE-BLOOD
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                      Bovinae; Bos
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MIM; 153622; -.
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
EXTRACELLULAR (POTENTIAL).
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MISSING (IN ISOFORM II).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARUFFO A., MELNICK M.B., LINSLEY P.S., SEED B.; "The lymphocyte glycoprotein CD6 contains a repeated characteristic of a new family of cell surface and se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD6_HUMAN STANDARD; PRT; 468 AA. P30203; (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 17-CELL DIFFERENTIATION ANTIGEN CD6 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
PIR;
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                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute by property institutions as its content are property institutions.
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Eukaryota; Metazoa; (
Eutheria; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00420; SP: PFAM; PF00530; SRCR;
                                                                   CARBOHYD
                                                                                                         DOMAIN
                                                                                                                                              CHAIN
                                                                                                                                                            SIGNAL
                                                                                                                                                                                     PFAM; PF00530;
                                                                                                                                                                                                                                                                                                                                                                                                      -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 92013796.
                                                                                                                       TRANSMEM
                                                                                                                                  DOMAIN
                                                                                                                                                                                                 PROSITE; PS00420;
                                                                                                                                                                                                                  MIM; 186720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARUFFO A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     931 LRLVDGGGPCGGRVEILDQGSWGTICDDDWDLDDARVVCRQLGCGEALNATGSAHFGAGS 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                   EXP. Med. 174:949-952(1991).

FUNCTION: INVOLVED IN CELL ADHESION.

SUBCELLULAR LOCATION: TYPE I MEMBRAN

SIMILARITY: CONTAINS 3 SRCR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E; X63723; CAA452; S19913; S19913; A46496; A46496;
                                                                                                                                                                                                                                                                                                                                                                      DATABASE: NAME-PROW; NOTE-CD guide CD6 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd6.htm"
                                                                                                                                                                         adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPIWLDDLNCTGKESHVWRCPSRGWGRHDCRHKEDAGVICS 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   മ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
52; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat.
1436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAA45255.1;
                                                                                                                                                                      SRCR; 3.
Glycoprotein;
                                                                                                                                                                                                SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.3%;
51.5%;
 Chordata; Craniata; Ven
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154196
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POTENTIAL.
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POTENTIAL.
                                                                                                                                                                         Transmembrane;
                                                                                                        POTENTIAL.
CYTOPLASMIC
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I MEMBRANE PROTI
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                                                                                                                                                                                                                                                                                                       There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata;
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PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                       Repeat; Signal.
                                                                                                                                                                                                                                                                                           Usage
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Best Local S
Matches 4
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Best Local
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                                                                                                                         CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DANGOTT L.J., JOKDAN "Cloning of the mRNA peptide speract.";
                                                                                                                                                             CARBOHYD
                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 8
-!- FUNCTION: RECEPTOR FOR THE
-!- SUBCELLULAR LOCATION: TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-AUG-1990 (Rel. 15, Created)
1-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
EGG PEPTIDE SPERACT RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPER_STRPU
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                          PFAM; PF00530; SRCR;
                                                                                                                                                                                                                                                                                                                                               EMBL; J04518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE; 89184581.
                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                       PROSITE; PS00420; SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euechinoidea; Echinacea;
324 TWAPIHTSFVMCTGVEDRLIDCILRDGWT-HSCYHVEDASVVCA 366
                         227
                                                 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 LRLVDGGGACAGRVEMLEHGEWGSVCDDTWDLEDAHVVCRQLG-CGWAVQALPGLHFTPG 219
                                                                                                                                                                                                                                                                                                                                     A32751; A3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGPIHRDQVNCSGAEAYLWDCPGLP-GQHYCGHKEDAGVVCS
                       IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKA--WHQAYFGE 284
                                                IRLMDGSGPHEGRVEIWHDDAWGTICDDGWDWADANVVCRQAGYRGAVKASGFKGEDFGF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSG-IAKAWHQAYFGEG 285
                                                                          49;
                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                       115
459
532
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                                                                          Conservative
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459
57820
                                                                                    38.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.Е.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                              Glycoprotein; Signal; Repeat
                                                                                                                         WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BELLET R.A.,
                                                                       Score 293; DB 1; Le
Pred. No. 6.69e-46;
14; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
15; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                         EGG PEPTIDE SPERACT RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86:2128-2132(1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGG PEPTIDE SPERACT.
I MEMBRANE PROTEIN
                                                                                                                         D27174AE CRC32;
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                                                                                                                                                                                                                        APPROXIMATE TANDEM REPEATS
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No. 1.30e-53;
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                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GARBERS D.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                           as its content
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                                                                                                Length 532
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P98074;
01-FEB-1996
                                                                Serine
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRSS7 OR ENTK.
Sus scrofa (Pig).
Sus scrofa; Metazoa; Chordata; Cran
                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS50068; LDLRA_2; 2.
PFAM; PF00057; ldl_recept_a; 2.
                                                                                                                                                                                                                                                                                                   PROSITE; PS00134; TRYPSIN_HIS; PROSITE; PS00135; TRYPSIN_SER; PROSITE; PS01180; CUB; 2.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D30799; BAA06459.1; -. HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ENTEROPEPTIDASE PRECURSOR (EC 3.4.21.9) (ENTEROKINASE)
                                                                                                          Signal-anchor;
                                                                                                                                   PFAM;
                                                                                                                                                                             PFAM;
                                                                                                                                                                                                                     PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HEAVY) CHAIN, AND A MINI CHAIN.

- I SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PPIM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURS CLEAVED BY A TRYPSIN-LIKE PROTEASE.

- I PIM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.

- I SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAI .

- I SIMILARITY: CONTAINS 1 SRCR DOMAIN.

- I SIMILARITY: CONTAINS 1 MAM DOMAIN.

- I SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROCARBOXYPEPTIDASES, AND PROELASTASES.

CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-1-ILE-7 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRYPSINOGEN.
SUBUNIT: HET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRYPSIN FAMILY.
                                                                                                                                                     PF00530;
PF00629;
                                                                                                                                                                                               PF00089;
                                                                                                                              PF01390;
                                                                                      protease;
    52
118
800
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HETEROTRIMER OF A CATALYTIC
                                                                                                      SEA; 1.
Glycoprotein;
                                                                                                                                                                                               trypsin; 1.
CUB; 2.
                                                                                                                                                       MAM;
                                                                                                                                                                           SRCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
    Zymogen;
117
799
1034
47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created;
Transmembrane: Repeat.
NON-CATALYTIC M CHAIN (MINI CHAIN)
NON-CATALYTIC H CHAIN (HEAVY CHAIN)
CATALYTIC L CHAIN (LIGHT CHAIN)
SIGNAL-ANCHOR (TYPE-II MEMBRANE PRO
                                                                                                             Myristate; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIGHT) CHAIN, A MULTIDOMAIN
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR (LYMPHOCYTE
                                                                                                                                                                                         CD5_
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01-NOV-1990
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                                                                                                     (LYMPHOCYTE
                                          Cetartiodactyla;
                                                         (Bovine).
Metazoa;
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POTENTIAL.

                                            Ruminantia;
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Pred. No. 3.64e-15;
24; Mismatches 40
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                                                         Craniata;
                                                                                                     CD5).
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Best Local 9
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p98073;
p1075-1996 (Rel. 33, Create Ol-FEB-1996 (Rel. 33, Last self-JUL-1998 (Rel. 36, Last alenterOpertidase precursor (E
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TRANSMEM
KITAMOTO Y., YUAN X., WU Q., MCCOURT D.W., SADLE "Enterokinase, the initiator of intestinal diges protease composed of a distinctive assortment of Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994)-1-FUNCTION: RESPONSIBLE FOR INITIATING ACTIVAT
                                                                              MEDLINE;
KITAMOTO
                                                                                                                                                                            KITAMOTÓ Y., VEILE R.A., DONIS-KELLER H., SA
"CDNA sequence and chromosomal localization
the proteolytic activator of trypsinogen.";
Biochemistry 34:4562-4568(1995).
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DOMAIN
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entities requires a license agreement (So
or send an email to license@isb-sib.ch).
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Nucleic Acids Res. 18:5296-5296(1990).

-i- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING PROLIFERATION. CD5 INTERACTS WITH CD72/LYB-2.

-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- SIMILARITY: CONTAINS 2 SRCR DOMAINS.
                                                                                                                                                                                                                                    MEDLINE; 95234679.
KITAMOTO Y., VEILE
                                                                                                                                                                                                                                                                                                                                                                                                PRSS7 OR ENTK
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PFAM; PF00530; SRCR
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YU Q., REICHERT M.,
                                                                                                                       TISSUE-DUODENUM
                                                                                                                                       SEQUENCE
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                                                                          94329561.
Y., YUAN X.,
                                                                                                                                       OF 749-1019
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etazoa; Chordata; Craniata; Vertebrata; Mammalia;
imates; Catarrhini; Hominidae; Homo.
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t annotation update)
(EC 3.4.21.9) (ENTEROKINASE).
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Pred. No. 7.27e-09;
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PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS50068; LDLRA_2; 2.
PFAM; PF00057; ldl_recept_a; 2.
PFAM; PF00059; LTypsin; 1.
PFAM; PF000431; CUB; 2.
PFAM; PF00431; CUB; 2.
PFAM; PF00529; MAM; 1.
PFAM; PF01390; SEA; 1.
PFAM; PF01390; SEA; 1.
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                       DISULFID
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Serine protease;
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DISEASE: DEFECTS IN PRSS7 CAUSE LIFE-THREATENING INTESTINAL DISEASE: DEFECTS IN PRSS7 CAUSE LIFE-THREATENING INTESTINAL MALABSORPTION CHARACTERIZED BY DIARRHEA AND FAILURE TO THRIVE. SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.

SIMILARITY: CONTAINS 2 CUB DOMAINS.

SIMILARITY: CONTAINS 1 MAM DOMAIN.

SIMILARITY: CONTAINS 1 MAM DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HETERODIMER OF A CATALYTIC (LIGHT) CHAIN AND A MULTIDOMAIN (HEAVY) CHAIN LINKED BY A DISULETIDE BOND. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE). TISSUE SPECIFICITY: INTESTINAL BRUSH BORDER. PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEOLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPE A). IT CATALYZES THE CONVERSION OF TRYPSINGEN TO TRYPSIN WITURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINGEN, PROCARBOXYPEPTIDASES, AND PROELASTASES.

CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-1-ILE-7 BONITRYPSINGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226200
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, MAM_2; 1.
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; LDLRA_2; 2.
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Transmembrane;
      MYRISTATE (POTENTIAL).
BY SIMILARITY.
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CHARGE
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NON-CATALYTIC CHAIN (HEAVY CHAIN).

CATALYTIC CHAIN (LIGHT CHAIN).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

LDL-RECEPTOR CLASS A 1.
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POTENTIAL.
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E RELAY SYSTEM
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         enterokinase.",

J. Protein Chem. 10:475-480(1991).

-i- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PROTEOLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CAPALYZES THE CONVERSION OF TRYPSINOGEN TO TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYP PROCARBOXYPEPTIDASES, AND PROELASTASES.
                                                                                                                                                        MEDLINE; 94043122.

LAVALLIE E.R., REHEMTULLA A., RACIE L.A., FERENZ C., GRANT K.L., LIGHT A., MCCOY J. FERENZ C., and functional expression of a c "Cloning and functional expression of a c subunit of bovine enterokinase.";

J. Biol. Chem. 268:23311-23317(1993).
                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ENTEROPEPTIDASE PRECURSOR (EC 3.4.21.9) (ENTEROKINASE)
                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
15-DEC-1999 (Rel.
                                                                                                  MEDLINE; 92189715.
LIGHT A., JANSKA H
                                                                                                                                                                                                                                              KITAMOTO Y., YUAN X., WU Q., MCCOURT D.W., SADLER J.E.; "Enterokinase, the initiator of intestinal digestion, is protease composed of a distinctive assortment of domains. Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
                                                                                                                                                                                                                          SEQUENCE OF 801-1035
                                                                                                                                                                                                                                                                                MEDLINE; 94329561.
KITAMOTO Y., YUAN X.,
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
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                                                                                    The amino-terminal sequence
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 CATALYTIC ACTIVITY:
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  OF.
  6-LYS-|-ILE-7 BOND IN
                       CHYMOTRYPSINOGEN
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TRYPSIN WHICH IN
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PROSITE; PS00740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS50068; LDLRA_2; 2.
PFAM; PF00057; ldl_recept_a; 2.
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PFAM; PF01390; SEA; 1.
Signal-anchor; Glycoprotein;
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PFAM;
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-!- TISSUE SPECIFICITY: INTESTINAL BRUSH BORDER.
-!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS CLEAVED BY A TRYPSIN-LIKE PROTEASE.
-!- SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.
-!- SIMILARITY: CONTAINS 2 COU DOMAINS.
-!- SIMILARITY: CONTAINS 1 SRCR DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS 3
                                                                                           CARBOHYD
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PROSITE: PS00135; TRYPSIN_SER;
PROSITE: PS01180; CUB; 2.
PROSITE: PS00740; MAM_1; 1.
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HSSP; P00763; 1DPO.
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SUBUNIT: HETI
MULTIDOMAIN
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L19663; AAA16035.1;
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PF00530; SRCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00089; tryps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease;
   HETERODIMER OF A CATALYTIC (LIGHT) CHAIN AND AIN (HEAVY) CHAIN LINKED BY A DISULFIDE BOND.
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en; Transmembrane; Repeat; Alternative splicing.
NON-CATALYTIC CHAIN (HEAVY CHAIN).
CATALYTIC CHAIN (LIGHT CHAIN).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LDL-RECEPTOR CLASS A 1.
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STRAIN-C57BL/6; TISSUE-DUODENUM;
STRAIN-C57BL/6; TISSUE-DUODENUM;
STRAIN-C57BL/6; TISSUE-DUODENUM;
SUBMITTED (DEC-1996) to the EMBL/GenBank/DBJ databases.
SUBMITTED (DEC-1996) to the EMBL/GenBank/DBJ databases.
SUBMITTED (DEC-1996) to the EMBL/GenBank/DBJ databases.
FOOTEOLYTIC PROENZMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE
A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN
TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN,
PROCARBOXYPEPTIDASES, AND PROELASTASES (BY SIMILARTY).
-!- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-(-ILE-7 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUL-1998 (Rel. 3
ENTEROPEPTIDASE (EK
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                                                           This SWISS-PROT entry is copyright. It is a between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                I- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR CLEAVED BY A TRYPSIN-LIKE PROTEASE (BY SIMILARITY).
I- SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.
I- SIMILARITY: CONTAINS 2 CUB DOMAINS.
I- SIMILARITY: CONTAINS 1 SRCR DOMAIN.
I- SIMILARITY: CONTAINS 1 MAM DOMAIN.
I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KN
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BC 3.4.21.9) (ENTEROKINASE).
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Pred. No. 1.78e-08;
21; Mismatches 35;
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(See http://www.isb-sib.ch/announce/

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287
                 781
                                  227
                                                723 VRFLNGTRSNNGLVQFNIHSIWHIACAENWTTQISNEVCHLLGL-GSANS-SMPISSTGG 780
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GP-VMLDEVRCTGNELSIE-QCPKSSWGEHNCGHK 319
                                IRLAGGSSVHEGRVELYHAGOWGTVCDDQWDDADAEVICROLGLSGIAKAWHQAYFGEGS 286
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BY SIMILARITY.
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CATALYTIC CHAIN (LIGHT CHAIN).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LDL-RECEPTOR CLASS A 1.
CUB.
                                                                  Score 120; DB 1;
Pred. No. 1.63e-07;
24; Mismatches 43
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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CD5_HUMAN STANDARD; PRT; 495 AA.
P06127;
O1-JAN-1988 (Rel. 06, Created)
O1-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR (LYMPHOCYTE T1/LEU-1), (LYMPHOCYTE ANTIGEN CD5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The B-cell surface protein CD72/Lyb-2 is the ligand for Nature 351:662-665(1991).

-i- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING T-CELL PROLIFERATION. CD5 INTERACTS WITH CD72/LYB-2.
-i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: COMTAINS 2 SRCR DOMAINS.
-i- DATABASE: NAME=PROW; NOTE=CD guide CD5 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd5.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JONES N.H., CLABBY M.L., DIA
HERZENBERG L.A., STROMINGER
"Isolation of complementary
glycoprotein T1/Leu-1.",
Nature 323:346-349(1986).
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X04391; CAA27979.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAN DE VELDE H., VON HOEGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 87014786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve:
Eutheria; Primates; Catarrhini; Hominidae;
277 RLVGGSSICEGTVEVRQGAQWAALCDSSSARSSLRWEEVCRE 318
|| ||||: || ||: :::||:::|| : ||:||:
228 RLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADA--EVICRQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH CD72/LYB-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR LEU1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6396; A26396
                                                                                                       Similarity
17, Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRCR;
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54625
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495
372
402
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133
133
382
                                                                                                                             14.8%;
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3ER J.L.,
ary DNA clones encoding the human lymphocyte
                                                                                                                                                                                                               Σ.
Σ
                                                                                                  Score 112;
Pred. No. 5.
11; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I., LUO W., PARNES J.R., CD72/Lyb-2 is the ligand
                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC
SRCR 1.
SRCR 2.
                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                             POTENTIAL.
8507C34C
                                                                                                                                                                                                                                                                                                                                                                                                               T-CELL SURFACE GLYCOPROTEIN CD5.
EXTRACELLULAR (POTENTIAL).
                                                                                                       Mismatches
                                                                                                                          DB 1; 1
.18e-06;
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                                                                                                                                                                                                             CRC32;
                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                          Length 495;
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THIELEMANS K.; for CD5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a collaboration - MBL outstation
                                                                                                       ζ,
                                                                                                  Gaps
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Search completed: Mon Mar Job time : 10 secs. 13 10:27:25 2000

US-09-147-947-6-04.rspt

************* (MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

բի_թթ protein - protein database search, using Smith-Waterman algorithm Mon Mar 13 10:27:42 2000; MasPar time 16.64 Seconds 420.878 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-09-147-947-6 (227-327) from US09147947A pep (4 of 6)

1 IRLAGGSSVHEGRVELYHAG.....KSSWGEHNCGHKEDAGVSCT 101

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl12
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Variance 61.971; scale 0.611

Statistics:

Mean 37.892;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

NO.	Score	Query Match	Length	DB	Ħ	Description	Pred. No.
1	450	59.4	2043	G	096943	SRCR DOMAIN, MEMBRANE	4.97e-82
N	427	56.4	2153	υı	097375	SCAVENGER RECEPTOR CYS	
ω	416		1116	4	Q07898	M130 ANTIGEN PRECURSOR	9.37e-74
4	416	•	1149	4	Q07901	M130 ANTIGEN, EXTRACEL	:
Մ	416	55.0	1151	4	Q07899	M130 ANTIGEN, CYTOPLAS	.37e-
σ	416	•	1156	4	Q07900	`	ω,
7	412	•	585	4	Q08380	•	.74e
œ	402	•	578	11	P70117	PANCREAS CANCER-ASSOCI	.30e-
9	402	•	1785	4	Q9Y211	DMBT1 PROTEIN.	2.30e-70
10	402	53.1	1785	4	Q9Y4V9	DMBT1/6KB.1 PROTEIN PR	.30e-
11	401	•	504	σ	Q28908	MUCIN (FRAGMENT).	.01e-
12	397		918	13	Q92098	PEMA-SRCR PROTEIN PREC	.71e
13	397		1594	σ	Q95218	HENSIN.	.71e-6
14	395		574	11	070513	MAMA.	3e-6
15	393	51.9	356	σ	097682	UNKNOWN MRNA, PARTIAL	3.42e-68
16	385	•	2083	11	Q6099 7	CRP-DUCTIN PRECURSOR (9e-6
17	384		577	11	Q07797	PEPTIDYLPROLYL ISOMERA	e-6
18	383		369	σ	Q29110	SCAVENGER-RECEPTOR PRO	.76e
19	383	50.6	895	13	Q9W6N1	LYSYL OXIDASE RELATED	9
20	383	50.6	1036	U	097378	SCAVENGER RECEPTOR CYS	. 76e

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01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

## MCIN (FRAGMENT). 21 381 50.3 600 6 028910 22 376 49.7 804 6 029113 23 374 49.4 480 6 029112 24 373 49.3 574 11 035649 25 370 48.9 437 6 029109 26 369 48.7 127 6 095316 27 368 48.6 774 4 094460 28 365 48.2 1299 11 062827 29 363 48.0 546 6 029111 30 356 47.0 347 4 043866 31 355 46.9 518 11 060754 32 346 45.7 528 5 097379 33 346 45.7 531 5 017064 35 341 45.0 48.3 11 099489 36 339 44.8 46.2 6 028881 37 38 44.6 754 11 035301 38 336 44.4 754 11 035301 39 329 43.5 352 11 035301 40 325 42.9 595 4 099448 41 325 42.9 601 4 099448 42 325 42.9 601 4 099448 45 318 42.0 822 13 099HC1 42 125 50	 											-	-		-	-	-				-	-				-	_		
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MUGIN (FRAGMENT). SCAVENGER-RECEPTOR PRO SCAVENGER-RECEPTOR PRO CYCLOPHILIN C-ASSOCIAT SCAVENGER-RECEPTOR PRO M130 ANTIGEN (FRACKENT LYSYL OXIDASE-RELATED EBNERIN. SCAVENGER-RECEPTOR PRO SCAVENGER RECEPTOR CYS P ALPHA. BACTERIA BINDING MACRO SCAVENGER RECEPTOR CYS SP85. LYSYL OXIDASE-LIKE PRO MACROPHAGE RECEPTOR AA MEMBRANE PROTEIN SCAVE MACROPHAGE RECEPTOR. LYSYL OXIDASE-RELATED SP-ALPHA. CD6E. CD6D. CD6D. CD6D. CD6D. CD6D. LYSYL OXIDASE HOMOLOG	13	4	4	4	4	11	11	11	4	σ	11	4	υī	σı	11	4	6	11	4	σ	σ	11	σ	σ	Φ				
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2. 65e - 65 4. 226e - 65 4. 226e - 65 2. 21e - 63 2. 21e - 63 2. 21e - 63 2. 21e - 63 2. 21e - 63 3. 49e - 62 2. 58e - 61 5. 49e - 62 3. 22e - 57 6. 23e - 57 6. 23e - 57 6. 23e - 57 6. 71e - 55 5. 91e - 55 5. 91e - 53 5. 91e - 53	LYSYL OXIDASE HOMOLOG	CD6B.	CD6D.	CD6C.	CD6E.	SP-ALPHA.	SP-ALPHA.	LYSYL OXIDASE-RELATED	MACROPHAGE RECEPTOR.	MEMBRANE PROTEIN SCAVE	MACROPHAGE RECEPTOR MA		SP85.	SCAVENGER RECEPTOR CYS	BACTERIA BINDING MACRO	SP ALPHA.	SCAVENGER-RECEPTOR PRO	EBNERIN.	LYSYL OXIDASE-RELATED	M130 ANTIGEN (FRAGMENT		CYCLOPHILIN C-ASSOCIAT			(FRAGMENT)				
	2.64e-50	5.91e-52	5.91e-52	5.91e-52	5.91e-52	6.71e-53	6.71e-53	1.48e-54	4.96e-55	2.87e-55	9.62e-56	3.22e-56	6.23e-57	6.23e-57	4.47e-59	2.58e-59	5.49e-61	1.83e-61	3.49e-62	.01e-6	.16e-6	.21e-6	•	.22e-6	.65e-6			,	•

•ALIGNMENTS

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9 9 9	RESULT	Qy	DЬ	Qy	DЪ	Ма	SO	אָל אָ	DR	RL	RT	RT	Z :	RA	RA X	RP	RN	8	88	0 0	DE	DT	DŦ	D i	A :	RESULI
01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)	LT 2 O97375. PRELIMINARY; PRT; 2153 AA.	287 GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSC 326	ACTGFENSLDECR	227 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286	IIYYQGVWGTVCDDSWGQPDADVVCRQLGYANI	Query Match 59.4%; Score 450; DB 5; Length 2043; Best Local Similarity 57.0%; Pred. No. 4.97e-82; Matches 57; Conservative 20; Mismatches 23; Indels 0; Gaps 0;	SEQUENCE 2043 AA; 220896 MW; 4CE19401 CRC32;	BEOSTTE: DECOMAGO: SEFERACT RECERTOR: 8		111:2635-2644(1998).	repeats.";	characterization of a molecule composed of scavenger receptor	ve sponge aggregation receptor.	I. MUELLER W.E.G.:	BLUMBACH B., PANCER Z., DIEHL-SEIFERT B., STEFFEN R., MUENKNER J.,	UENCE		idae; Geodia.	Eukarvota: Metazoa: Porifera: Demospongiae: Tetractinomorpha:	SRCRM2.	MEMBRANE FORM 2.	12, Last	(TrEMBLIE 10.	(TrEMBLrel.		LT 1 OGGGA3 PRELIMINARY: PRT: 2043 AA

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PRESULT
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AC 007898;
DT 01-NOV-19;
DT 01-NOV-19;
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DE M130 ANTICO
GN CD163
OC ENARTYOTA
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OC ENTRY
RN MEDLINE;
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Best Local (
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SIGNAL
CHAIN
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EMBL;
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PANCER Z., RAST J., DAVIDSON E
"EVOLUTION of the Immune Syste
Genes of the Mammalian Immune
Coelomocytes.";
                                                                                                                                                                                            EMBL;
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MASON D.Y.;

A new macrophage differentiation antigen scavenger receptor superfamily ";

Eur. J. Immunol. 23:2320-2325(1993).
                                                                  EMBL;
                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
RITTER M., BUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAW S.A., MICKLEM K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 93380506.
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Homo sapiens (Human).
Chordata;
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EMBL; AF064259; AAD08654.1; -.
PROSITE; PS00420; SPERACT_RECEPTOR;
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                                                                                                                                                                                                                                                                                                                                           Genomic organization
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                      Y18394;
Y18395;
Y18396;
Y18397;
Y18398;
Y18399;
Y18400;
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Y18393;
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56; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Metazoa; Chordata; C:
Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                     rganization of the human CD163 gene."; (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                    BUECHLER C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
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                                                                                                                                               CAB45233.1;
CAB45233.1;
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                                                                                                                              CAB45233.1;
CAB45233.1;
                                                                                                                                                                                                                                                                                                    CAA80541.1;
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2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purpuratus (Purple sea urchin).
; Echinodermata; Echinozoa; Echinoidea;
nacea; Echinoida; Strongylocentrotidae;
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Pred. No. 2.00e-76;
23; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata;
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SEQUENCE
                                                                                            Q07899 PRELIMINARY; PRT; 1151 AA. (207899); Ol-NOV-1996 (TrEMBLrel. 01, Created) Ol-NOV-1996 (TrEMBLrel. 01, Last sequence update) Ol-NOV-1999 (TrEMBLrel. 12, Last annotation update) M130 ANTIGEN, CYTOPLASMIC VARIANT 1 PRECURSOR.
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Q07901;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 12, Last annotation update)
M130 ANTIGEN, EXTRACELLULAR VARIANT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y18402; CAB45233.1; JOIN EMBL; Y18403; CAB45233.1; JOIN PFAM; PF00530; SRCR; 9. PRINTS; PR00258; SPERACTRCPTR.
                                                           Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                           1017
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Eukaryota; Metazoa; C
  SEQUENCE FROM N.A.
                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Eur. J. Immunol. 23:2320-2325(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00530;
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56; Conservation
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56; Conser
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1149 AA;
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A; 120979 MW;
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Catarrhini;
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Pred. No. 9.
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MW; 4901C708 (
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M130 ANTIG
                                            Craniata; Ve
i; Hominidae;
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.37e-74;
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                                                                Vertebrata;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
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MEDLINE; 93380506.
LAW S.A., MICKLEM K.J.,
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01-NOV-1999 (TrEMBLrel. 12, Last annotation up
M130 ANTIGEN, CYTOPLASMIC VARIANT 2 PRECURSOR.
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PFAM; PF00530; SRCR; 9.
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LAW S.A., MICKLEM
MASON D.Y.;
                                                                                                      Q08380
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Eur. J. Immunol. 23:2320-2325(1993).
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les 56; Conser
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  BINDING
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Z22969; CAA80542.1; -.
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1156 AA;
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1151 AA;
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  PROTEIN PRECURSOR
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19; N
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Pred. No. 9.37e-74;
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Pred. No. 9.37e-74;
19; Mismatches 26;
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M130 ANTIGEN,
MW; 287A07A0 C
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M130 ANTIGEN, CYTOPLASMIC VARIANT
W; A72EDD2F CRC32;
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J. Biol. Chem. 268:14245-142/0/1000
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SIGNAL
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ULLRICH A.,
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J. Biol. Chem. 269:18401-18407(1994).
EMBL; L13210; AAA36193.1; -.
EMBL; X79089; CAA55699.1; -.
PFAM; PF00530; SRCR; 1.
                                                                                                                                                                                                                                            SEQUENCE
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PROSITE; PS00420; SPERACT.
PFAM; PF00530; SRCR; 1.
PRINTS; PR00258; SPERACTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1997 (TremBirel. 02, Created)
01-FEB-1997 (TremBirel. 02, Last sequence up
01-WOV-1999 (TremBirel. 12, Last annotation
PANCREAS CANCER-ASSOCIATED PROTEIN 4.
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                                                                                                                                     Local Similarity 52.5%; res 53; Conservation
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                                                                                      24 MRLVNGASANEGRVEIFYRGOWGTVCDNLWNILDANVVCRALGYENATQALGRAAFGPGR 83
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GPVMLDEVECTGTEPSLANCSSLGWLKSRCGHEKDAGVVCS 124
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                                                          IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
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54; Conser
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585 AA;
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A; 64398 MW;
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53.5%;
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                                                                                                                                                 Score 402; DB 11; Pred. No. 2.30e-70; 15; Mismatches 33;
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Pred. No. 8.74e-73;
19; Mismatches 28;
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MAC-2 BINDING PROTEIN.
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Eukaryota; Metazoa;
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AB020839;
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AB020834;
AB020835;
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AB020830;
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AB020827;
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AB020818;
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AB020825;
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52; Conser
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Last sequence up
Last annotation
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Pred. No. 2.30e-70;
19; Mismatches 30
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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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13; Mismatches 21;
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01-NOV-1999 (TrEMBLrel. 12, Last annotation

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GRVEIYHGGRWGTVCDDSWDTQDAQVVCRQLQCGDAVSAPGGAYFGSGSGPITLDDVNCS 1140
                             Score 397; DB 6;
Pred. No. 3.71e-69;
12; Mismatches 25
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Conservative

52.4%;

MEDLINE: 97096804.
TAKITO J., HIKITA C.,

AL-AWQATI Q.;

SEQUENCE FROM N.A. MEDLINE; 97096804.

"Hensin, a new collecting duct protein involved plasticity of intercalated cell polarity.";
J. Clin. Invest. 98:2324-2331(1996).
EMBL; AF043112; AAD02242.1; -.
HSSP; P29392; ISFP.
PROSITE; PS00420; SPERACT_RECEPTOR; 6.
PFAM; PF00530; SRCR; 2.
SEQUENCE 1594 AA; 172763 MW; 34EB5962 CRC32;

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PEMA-SKUR FRANKLIS (Sea lamprey).
Petromyzon marinus (Sea lamprey).
Eukaryota; Metazoa; Chordata; Craniata; Cephalaspidomorphi;
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J. Clin. Endocrinol. Metab. 8
EMBL; AF105035; AAC97514.1;
HSSP; P29392; 1SFP.
NON_TER 356 356
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98439602.
ACE C.I., OKULICZ W.C.
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A progesterone-induced
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356 AA;
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Pred. No. 3.42e-68;
22; Mismatches 28;
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16; Mismatches 33
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Qy Вр

Matches Query Match Best Local

Similarity 58; Conser

Conservative

52.4%;

Score 397; DB 13; Pred. No. 3.71e-69; 14; Mismatches 27;

RL DR DR DR DR DR DR DR FT FT FT SQ

Signal.

SEQUENCE

1 25 918

.24 PO 918 PE 101417 MW;

POTENTIAL.
PEMA-SRCR PROTEIN.
N; 66F9C10E CRC32;

AA;

EMBL: 020652; AAA90990.1; -. HSSP: P08709; 1BF9.
PFAM: PF000008; EGF; 4.
PFAM: PF000530; SRCR: 2.
PFAM: PF00100; zona_pellucida; 1
PRINTS: PR00258; SPERACTRCPTR.

MAYER W.E., TICHY H.;
"A cDNA clone from the sea lamprey scavenger receptor Cys-rich (SRCR)
Gene 164:267-271(1995).

SIRALN=22P; TISSUE=INTESTINE; MEDLINE; 96069593.

SEQUENCE FROM N.A.

δõ Вb

286 524 227

RESULT

Q95218

PRELIMINARY;

PRT;

1594

A

095218; 095219; 01-FEB-1997 (TTEMBLrel. 02, Created) 01-FB-1999 (TTEMBLrel. 10, Last sequence up 01-NAY-1999 (TTEMBLrel. 12, Last annotation

Oryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Cra Eutheria; Lagomorpha; Leporidae;

Oryctolagus

HENSIN

Qy 227 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286

Дb

Qy

Search completed: Mon Mar 13 10:28:00 2000 Job time : 18 secs.

****************** (TM)

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protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 13 10:25:04 2000; MasPar time 10.24 Seconds 465.385 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-147-947-6 (117-217) from US09147947A.pep (3 of 6)

Sequence: 1 VRLRGGKNEFEGTVEVYASG.....KDIWQGGVCPQKMAAAVTCS 101

Scoring table: PAM 150 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

pir62 Fipir1 2:pir2 3:pir3 4:pir4

Database:

Statistics:

Mean 37.928; Variance 60.892; scale 0.623

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Query Match	Length	DB	ID	Description	Pred. No.
_	324	2	761	ນໍ່	57	brain-specific serine	.42e-5
2	266	4	2153	N	489	cavenger receptor c	.72e-3
w	256	33.5	454	N	I46862	e scavenge	9
4	251	2	1116	N	607	antigen - huma	.15e-3
C1	251	N	1149	N	œ	antigen (e	.15e-3
σ	251	2	1151	Ŋ	æ	antigen (cytoso	.15e-3
7	251	Ν.	1156	N	9	e O	.15e-3
ထ	248		454	N	4	sca	.71e-3
9	244	1	458	Ν	B44407	SC	.79e-3
10	239	1	518	Ν	A55840	macrophage bacteria-b	.77e-3
Ξ	237	۳	451	N	84		.95e-3
12	236	0	1436	N	64	1.1 precu	.31e-3
13	234	0	600	N	S56744	clone p	.49e-3
14	233	0	453	N	82	LDL receptor I, macro	.61e-3
15	230	0	918	N	43	ptor c	.79e-3
16	219	8	585	N	71		.45e-2
17	212	7.	1290	N	71	Sor -	.26e-2
18	206	7.	504	N	67	one pGM31-1	.04e-2
19	205	6.	626	N	91	precursor - m	.41e-2
20	202	5	577	N	Ω	philin C-assc	.59e-2
21	193	5	532	N	275	eceptor pre	.56e-2
22	188	4.	468	N	σ	qlycoprote	. 95e-2
23	113	4.	1035	-	4309	~	.45e-

110 14.4 1488 2 C70984 probable ppsE protein 107 14.0 1034 1 A53663 enteropeptidase (EC 3 106 13.9 1489 2 S73015 polyketide synthase p 105 13.7 1019 1 A56318 enteropeptidase (EC 3 102 13.4 583 2 A29154 croeplement factor I (45	44	43	42	41	40	39	ა 8	37	36	3 5	34	3 3	32	31	30	29	28	27	26	25	24
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C70984 probable ppsE protections (EC S73663) polyketide synthase A56318 enteropeptidase (EC A29154 enteropeptidase (EC A29154 enteropeptidase (EC A29154 enteropeptidase (EC A29154 enteropeptidase) enteropeptidase (EC A29154 enteropeptidase) enteropeptidase (EC A29154 enteropeptidase) enteropeptidase (EC A29079 enteropetion enter	1857	1014	1719	1113	558	495	381	699	604	527	491	1751	613	494	442	558	495	583	1019	1489	1034	1488
probable ppsE prote enteropeptidase (EC polyketide synthase enteropeptidase) (EC complement factor I T-cell surface glyc hypothetical protein - 1 years (1900 protein - 1 year	Н	N	2	N	N	-	N	Ν	2	Ν	N	H	N	μ	N	Ν	ш	N	ш	N	Н	N
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	fatty-acid synthase (hypothetical protein	retinoblastoma-associ	low-density lipoprote	nuclear factor-kappa	surface	ryl-	F17	hypothetical protein	'n	HMGS protein - yeast	laminin alpha-2 chain		lymphocyte surface gl	tein -	hypothetical protein	T-cell surface glycop	O	idase (EC	synthase	ptidase	ppsE prote

ALIGNMENTS

Db 225 SGPILLDEVRC	Db 166 IRLVGGNSGHE 	Query Match 42.4%; Best Local Similarity 45.5%; Matches 46; Conservative	386-486 513-516 517-755 93,521,569 562,612,711 #len	85-157 163-266	CLASSIFICATION #sup cy KEYWORDS glyc FEATURE	##molecule_type mRNA ##residues 1-76 ##cross-references D ##experimental_sourc	reference	#duchors raind TS #journal Bioc #title Mole		ENTRY JC5759 TITLE brain- ORGANISM #forma DATE 24-Jan
SGPILLDEVRCTGNEMSIEQCPKSSWGEHNCGHKEDAGVSC 265	IRLVGGNSGHEGRVELYHAGO¶GTICDDQWDNADADVICRQLGLSGIAKAWHQAHF-GEG 224: :: :	42.4%; Score 324; DB 2; Length 761; ty 45.5%; Pred. No. 6.42e-53; servative 19; Mismatches 34; Indels 2; Gaps 2;	#domain scavenger receptor cysteine-rich #status predicted #label SRC\ #domain furin binding #status predicted #label FRB\ #domain trypsin homology #label TRY\ #binding_site carbohydrate (Asn) (covalent) #status predicted\ #active_site His, Asp, Ser #status predicted #active_site His, Asp, Ser #status predicted #length 761 #molecular-weight 84136 #checksum 5449	#domain kringle-like #status predicted #label KRI\ #domain scavenger receptor cysteine-rich domain homology #label SRC7\	#superfamily trypsin homology; scavenger receptor cysteine-rich domain homology glycoprotein; hydrolase; serine proteinase	#molecule_type mRNA #residues 1-761 ##label YAM #cross-references DDBJ:D89871 #experimental_source brain	with a kringle-like structure and three scavenger receptor cysteine-rich motifs. s MUID: 98008848	Idmamura, I.; IdmaSILIO, K.; ISULUOXA, N.; NAKAZATO, H.; TSUJimura, A.; Yamaguchi, N. Biochem. Biophys. Res. Commun. (1997) 239:386-392 Molecular cloning of a novel brain-specific serine professe	af-1999	JC5759 #type complete brain-specific serine proteinase (EC 3.4.21) - mouse #formal_name Mus musculus #common_name house mouse 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change

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353 VRLVGGRGPHEGRVEILHNGQWGTVCDDHWELRAGQVVCRSLGYRGVKSVHKKAYF-GQG 411
                                                                                                                                                                                                                                                                           preliminary; translated ##molecule_type mRNA ##rpeidnon
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                                                                                                                                                                                                                           ##residues 1-454 ##label BIC 1-454 ##label BIC ##cross-references GB:L11693; NID:g165508; PIDN:AAA31402.1; PID:g165509 ##CRATION #superfamily unassigned collagens; scavenger receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-2153 ##label PAN
##cross-references EMBL:AF064259; NID:g4165052; P.ID:g4165053
PIDN:AAD08654.1
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nes 42; Conservative
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Similarity 38.6%;
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J. Clin. Invest. 41992 90:1450-1457
Rabbit aortic smooth muscle cells express
macrophage scavenger receptor messenger
from endothelial cells.
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Origins of immunity: transcription factors and homologs of effector genes of the vertebrate immune system expressed
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urchin (Strongylocentrotus purpuratus)
#formai_name Strongylocentrotus purpuratus #common_name
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#formal_name Oryctolagus cuniculus #common_name domestic
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#length 2153 #molecular-weight 226556
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                                               Score 256; DB 2;
Pred. No. 7.99e-37;
17; Mismatches 40
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Pred. No. 3.72e~39;
22; Mismatches 40
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##residues 1-1116 ##label RES
##cross-references EMBL.222968; NID:9312141; PID:9312142
##CTOSS-references EMBL.222968; NID:9312141; PID:9312142
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Local Similarity 39.8%;
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M130 antigen (extracellular variant) - human
#formal_name Homo sapiens #common_name man
17-May-1996 #sequence_revision 17-May-1996 #:
02-Aug-1996
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Bur. J. Immunol. (1993) 23:2320-2325

A new macrophage differentiation antigen which the scavenger receptor superfamily.
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Pred. No. 1.15e-35;
18; Mismatches 40
                                                 K.J.; Shaw,
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KEYWORDS
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Matches 41; Conservative
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Eur. J. Immunol. (1993) 23:2320-2325
A new macrophage differentiation antigen which is a member o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138004 #type complete
M130 antigen (cytosolic variant 1) - human
#formal_name Homo sapiens #common_name man
17-May-1996 #sequence_revision 17-May-1996 #text_change
07-Feb-1997
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Pred. No. 1.15e-35;
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Db 924 IRLQEG : :	Query Match Best Local Sim Matches 41;	816-920 921-1024 SUMMARY	75-67 11-81	151-254 258-361 365-468 470-573	##TOLECULE ##ROLECULE ##ROLECULE ##ROLECULE ##ROLECULE CLASSIFICATION KEYWORDS FEATURE 43-147	#journal #title #cross-refere #accession	RESULT 7 ENTRY TITLE ORGANISM DATE ACCESSIONS REFERENCE #authors	Db 924 IRLQEG	Query Match Best Local Simil Matches 41;	470-573 575-678 711-814 816-920 921-1024 SUMMARY
PTSCSGRVEIWHGGSWGTVCD	32.9%; Score 251; DB 2; Length 1156; nilarity 39.8%; Pred. No. 1.15e-35; Conservative 18; Mismatches 40; Indels 4; Gaps 4;	receptor cysteine-rich domain receptor cysteine-rich domain ar-weight 125352 #checksum 904	SRCS\ SRCS\ SRCS\ SCavenger receptor cysteine-rich domain		# abel SRC1\ Light mana presentable and present the present property of the p	Eur J. Immunol. (1993) 23:2320-23 A new macrophage differentiation a the scavenger receptor superfami nces MUID:93380506	I38005 #type complete M130 antigen (cytosolic variant 2) - human #formal_name Homo sapiens #common_name man 17-May-1996 #sequence_revision 17-May-1996 #text_change 07-Feb-1997 I38005; S36079 I38003 Law, S.K.; Micklem, K.J.; Shaw, J.M.; Zhang, X.P.; Dong, Y.; Willis, A.C. Mason, D.Y.	IRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQVVCQQLGCGPALKAFKEAEF-GOG 982 : : : : ::	32.9%; Score 251; DB 2; Length 1151; nilarity 39.8%; Pred. No. 1.15e-35; ; Conservative 18; Mismatches 40; Indels 4; Gaps 4;	#domain scavenger receptor cysteine-rich domain homology #label SRC5\ #domain scavenger receptor cysteine-rich domain homology #label SRC6\ #domain scavenger receptor cysteine-rich domain homology #label SRC1\ #domain scavenger receptor cysteine-rich domain homology #label SRC1\ #domain scavenger receptor cysteine-rich domain homology #label SRC8\ #domain scavenger receptor cysteine-rich domain homology #label SRC9 #label SRC9 #label SRC9 #label SRC9 #label SRC9 #label SRC9 #label SRC9 #label SRC9 #label SRC9 #length 1151 #molecular-weight 124820 #checksum 1481

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Best Local Similarity 39.8%;
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                                                                                                                      #accession
##experimental_source macrophage-like cell line P388D
                                          ##status preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 1.458 ##label DOI
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macrophage scavenger receptor type I
#formal_name Mus musculus #common_name house mouse
30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
20-Sep-1999
                                                                                                                                                                                     Doi, T.; Higashino, K.; Kurihara, Y.; Wada, Y.; Miyazaki, T. Nakamura, H.; Vesugi, S.; Imanishi, T.; Kawabe, Y.; Itakura, H.; Yazaki, Y.; Matsumoto, A.; Kodama, T. J. Biol. Chem. (1993) 268:2126-2133

Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger
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ENTRY
TITLE
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                                                                       KEYWORDS
                                                                                                                 CLASSIFICATION
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                                                                                                         ##residues 1-518 ##label ELO
##cross-references GB:U18424; NID:9682722;
IFICATION #superfamily scavenger receptor
                                                                                                                                                                                            ##molecule_type mRNA
##residnor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 TGPI-WLNEVMCFGRESSIENCKINQWGVLSCSHSEDAGVTCT 457
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##cross-references GB:L04274; NID:g293745; PIDN:AAA39747.1; PID:g293746
#FICATION #superfamily unassigned collagens; scavenger receptor
cysteine-rich domain homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 VRLVGGSGAHEGRVEIFHQGQWGTICDDRWDIRAGQVVCRSLGYQEVLAVHKRAHF-GQG 415
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Similarity 36.9%;
38; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                    Cloning of a novel bacteria-binding receptor structurally related to scavenger receptors and expressed in a subse
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Structures and high and low affinity ligand binding
properties of murine type I and type II macrophage
scavenger receptors.
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An ancient, highly conserved family of cysteine-rich protein domains revealed by cloning type I and type II murine macrophage scavenger receptors.
                                                                           transmembrane protein
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Cell (1995) 80:603-609
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macrophage bacteria-binding receptor MARCO - mouse
#formal_name Mus musculus #common_name house mouse
23.Mar-1995 #sequence_revision 05-Apr-1995 #text_cl
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Sormunen, R.;
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#label SRC
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R.; Liakka,
   scavenger
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Pred. No. 4.79e-34;
19; Mismatches 42
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   receptor
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A.; Thesleff,
   cysteine-rich
                                                                                                             PID:g682723
cysteine-rich
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I.; Kraal,
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domain homology
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176 LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS

217

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KEYWORDS
FEATURE
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Best Local
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Best Local Similarity 39.2%;
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Matsumoto, A.; Naito, M.; Itakura, H.; Ikemoto, S.; Asaoka, H.; Hayakawa, I.; Kanamori, H.; Aburatani, H.; Takaku, F.; Suzuki, H.; Kobari, Y.; Miyai, T.; Takahashi, K.; Cohen, E.H.; Kydro, R.; Housman, D.E.; Kodama, T. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9133-9137
#title expression, and localization in atherosclerotic lesions.
#cross-references_MUID:91067661
                                                                                                                                                                                                                                                                                                                                                                                                                               #gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coession A44408
##status preliminary; not compared with conceptual translation
##molecule_type nucleic acid
##residues 155-272 ##label EMI hackbone (NCBIP:123189)
                      409
                                                                117
                                                                                                                                                                                                                                                                                                                                                                                       ##cross-references GDB:128046; OMIM:153622
p_position 8p22-8p22
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TGPI-WLNEVFCFGRESSIEECKIROWGTRACSHSEDAGVTCT
                                                              VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGG-KGIAKQTPFSGLG 175
                                                                                                      VRLVGGSGPHEGRVEILHSGQWGTICDDRWEVRVGQVVCRSLGYPGVQAVHKAAHF-GQG 408
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                                                                                                                                               31.0%;
Similarity 37.9%;
39; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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Structure, organization, and chromosomal mapping of the human macrophage scavenger receptor gene.
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macrophage scavenger receptor splice form I - human
#formal_name Homo sapiens #common_name man
28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change
20-Sep-1999
                                                                                                                                                                                                                                                                                                                        alternative splicing; coiled coil;
                                                                                                                                                                                                                                                                                                                                                                 *superfamily unassigned collagens; scavenger receptor
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#length 518 #mole
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                                                                                                                                               Score 237; DB 2; Length 451
Pred. No. 1.95e-32;
17; Mismatches 43; Indels
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Pred. No. 6.77e-33
21; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from NCBI backbone
                                                                                                                                                                                                                                                                                                                      transmembrane protein
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#cross-references MUID:94194107
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##residues 1-1436 ##label
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##cross-references EMBL:X63723; NID:g13; PID:g14
##experimental_source CD4-CD8- gamma delta T lymphocytes
##note sequence extracted from NCBI backbone (NCBIP:117475)
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h 30.9%;
Similarity 37.9%;
39; Conservative
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Members of the novel WCl gene family are differentially expressed on subsets of bovine CD4-CD8- gamma delta Texpressed.
                                                                   #label SR11
#length 1436 #mol
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Molecular characterization of the WC1 antigen specifically on bovine CD4-CD8- gamma delta ces MUID:93056489
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#label SR10\
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1.1 precursor
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20; 1
                 Score 236;
Pred. No. 3.
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e 236; DB 2; Lo
. No. 3.31e-32;
Mismatches 40;
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                                  Length 1436;
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#title
                                                                                                                                                                                Matsudaira, P.; Krieger, M.

#journal Nature (1990) 343:531-535

#title Type I macrophage scavenger receptor contains

and collagen-like colled colls.

#cross-references_MUID:90136965
                                                                                                                                                                    #accession
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#creating sequences: evidence for scavenger receptor cysteine-rich repeats.

#social Scavenger sequences: evidence for scavenger security sequences: evidence for scavenger security sequences: evidence for scavenger security sequences: evidence for scavenger security sequences: oss-references MUID:95374471
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                                                                                                                                                 ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 SGPILLDDVGCSGYETYLWSCSHSPWNSHNCGHSKDASVICS 483
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                                                                                                        ##residues
                                                                                                                        ##molecule_type mRNA
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Similarity 38.2%;
39; Conservation
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LDL receptor I, macrophage - bovine
macrophage scavenger receptor type I

#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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    #superfamily unassigned collagens;
                                                                                                                                                                  S08276
                                                                                                                                                                                                                                                                                    Kodama, T.; Freeman, M.; Rohrer, L.; Zabrecky,
                                                                                                                                                                                                                                                                                                                                S0827
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mucin (clone pGM7-1) - bovine (fragment)
#formal name Bos primigenius taurus #common_name cattle
27_oct-1995_#sequence_revision 30-Jan-1998 #text_change
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                                                                                                        1-453 ##label KOD
                                           part of this sequence was confirmed
                                                                                                                                           not compared with conceptual translation
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#label SRC4
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#label SRC3\
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#domain scavenger receptor cysteine-rich domain #label SRC2\
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Pred. No. 9.49e-32;
18; Mismatches 43
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    scavenger
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349-452
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                                     Query Match
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Best Local Similarity 37.9%;
Matches 39; Conservative
                                                                                                                                      876-895
896-918
40,545,5
                                                                                                                                                                                                                        234-267
295-328
356-389
410-443
463-565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Mayer, W.E.; Tichy, H.
#journal Gene (1995) 164:267-271
#title A cDNA clone from the sea lamprey Petromyzon marinus coding
for a scavenger receptor Cys-rich (SRCR) domain protein.
#cross-references MUID:96089593
#accession JC4361
                                                                                                                                                                                                                                                                                                                                                                55-157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1.918 ##label MAY
##cross-references GB:UZ0652; NID:g790233; PID:g790234
This protein is rich in cysteine and plays a role
contacts and cell activation or differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
##residues 1-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 TGPI-WLNEVFCFGKESSIEECRIRQWGVRACSHDEDAGVTCT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQL-GGKGIAKQTPFSGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 VRLVGGSGPHEGRVEIFHEGQWGTVCDDRWELRGGLVVCRSLGYKGVQSVHKRAYF-GKG 410
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                                                                                                                                          ,575,585,
                    Similarity
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                                                                          predict
#length 918 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein; growth factor; receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *superfamily EGF homology; scavenger receptor cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JC4361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #formal_name Petromyzon marinus #common_name sea lamprey
08-Jan-1996 #sequence_revision 08-Feb-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scavenger receptor Cys-rich epidermal growth factor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #length 453 #mo
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain homology
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    sea lamprey

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                                                                                                                                                                                                                                                                                                                                                                               #product scavenger receptor Cys-rich epidermal growth
  factor #status predicted #label MAT\
                                                                                                                   #binding_site carbohydrate (Asn)
                                                                                                                                                          #domain transmembrane #status predicted #label IMM\
                                                                                                                                                                                                                      #domain scavenger receptor cysteine-rich domain homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #binding_site carbohydrate (Asn) (covalent) #status
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              30.1%;
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                                                                              #molecular-weight 101417 #checksum 2936
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Pred.
17; M
                  Score 230; DB 2;
Pred. No. 7.79e-31;
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Pred. No. 1.61e-31;
18; Mismatches 42;
  Mismatches
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EG2/
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                                       Length 918;
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Gaps
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dď protein - protein database search, using Smith-Waterman algorithm

Tabular output Run on: not generated. Mon Mar 13 10:26:03 2000; MasPar time 4.59 Seconds 284.891 Million cell updates/sec

ALIGNMENTS

Description: Perfect Score: Title: >US-09-147-947-6 (117-217) from US09147947A.pep (3 of 6) 764

Sequence: 1 VRLRGGKNEFEGTVEVYASG......KDIWQGGVCPQKMAAAVTCS 101

Scoring table: PAM 150 Gap 11

Searched:

131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 26.677; Variance 101.261; scale 0.263

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Query Match	Length I	DB.	ID	Description	Pred. No.
ŢŢ) 239	<u>'</u> ;	489	N	US-08-794-	Sequence 7, Applicatio	6.02e-15
×	239	1.	518	μ	US-08-392-	uence 2, Applicat	.02e-
ω	237	31.0	451	w	CT-US96	2, Appl	0e-
4	237	۲	451	ب	8-4	2, Appl	.70e-
ហ	237	۳	451	N	US-08-948-	2, Appl	
o,	237	μ.	451	Ν	US-08-973-	2, Appl	.70e-
7	237		451	_	US-08-154-	2, App	.70e-
8	224	9	453	4	5510466-4	o. 55104	.13e-
9	219	œ	585	N	US-08-316-	ce 10	.96e-1
10	219		585	H	US-08-477-	Sequence 10, Applicati	.96e-
11	219	œ	585	μ,	US-08-473-	, App	.96e-1
12	217	ω.	495	N	US-08-794-	e 2, Þ	•
13	217		520	N	US-08-794-	9	.12e-1
14	212	7.	1290	۳	US-08-470-	2, App	.63e-1
15	113	14.8	798	μ,	US-08-200-	Sequence 2, Applicatio	.93e-0
16	113	4	798	ω	PCT-US94-0	'n	.93e-
17	88	11.5	1130	4	5444158-2	o. 5444	.31e+
18	88	٠	1130	N	US-08-125-	Sequence 2, Applicatio	31
19	88		1130	2	US-08-460-	2	ω ω
20	88	11.5	3111	N	US-08-125-		ω .ω
21	88		3111	N	US-08-460-	4,	ω
22	83	•	268	2	US-08-353-	e 65	8.8
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4.1	44	4 3	42	41	40	S S	38	37	36	35	34	ω ω	32	ω μ	30	29	28	27	26	25	24	4
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PCT-US93-0	500	US-08-353-	US-08-353-	US-09-047-	5260223-1	-08-62	US-08-420-	US-08-543-	US-08-680-	PCT-US95-0	US-08-310-	US-08-712-	US-08-804-	us-08-896-	US-08-896-	us-08-290-	US-08-290-	US-08-681-	US-08-399-	US-08-459-	US-08-399-	
Sequence	Compace	Sequence	Sequence	Seguence	Patent No.	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
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INFORMATION FOR SEQ ID NO: 7:	TELEFRAX: 610-270-4026	ATTON	-	TRATION NUMBER: 34,3	NAME: Han, William T	/AGENT 1		ICATION NO	PRIOR APPLICATION DATA:	CLASSIFICATION: 435	: 04-FEB-199		LICATION DATA:	FastSEO	OPERATING SYSTEM: DOS	7) 10 H	MEDITIM TRUES: Diskette	DEPONDE F	-4	4	: PA	King of Prussia	09 Swedeland Road	ADDRESSEE: SmithKline Reecham Corporation	コガスつぎ かつしゅずのの	֓֞֜֜֜֜֜֜֜֜֜֜֜֓֓֓֓֓֜֜֜֜֜֓֓֓֓֓֜֜֜֜֜֜֓֓֓֓֓֓		OF INVENTION: Himan Macro compager	GLUSS,	Audillou,	Elshour.	RMATION:	Patent No. 5916766	Sequence 7, Application US/08794795		Sequence 7, Application US/08794795			xxxxxx	US-08-794-795-7 STANDARD; PRT; 489 AA.	LT 1

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              Patent No. 5691197
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 VRIMGGTNR--GRAEVYYNNEWGTICDDDWDNNDATVFCRMLGYS-RGRA-LSSYGG-GS 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 GNI-WLDNVNCRGTENSLWDCSKNSWGNHNCVHNEDAGVECS 489
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                     TELEX: (216) 98 INFORMATION FOR SEQ
                                                                                                                                                             SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                          ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: 720 Kb s
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kangas, Maarit
TITLE OF INVENTION: An Insolated DNA Sequence For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 489 AA; 49441 MW; 1141296 CN;
            SEQUENCE CHARACTERISTICS
                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (216) 861-5582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 489 a TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217
                                                                                                                                                                                                                                                                                           STREET:
                                                                                         NAME: Minnich, Richa
REGISTRATION NUMBER:
                                                                                                                           FILING DATE: CLASSIFICATION:
                                            TELEFAX:
                                                                             REFERENCE/DOCKET NUMBER: TRV 2 009
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                         COUNTRY:
LENGTH:
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fay, Sharpe, Beall, Fagan
ADDRESSEE: Minnich & McKee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
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ilarity 39.2%;
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                                              (216) 241-1666
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                                                                                                                                                                         Word Perfect 5.1
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a Collagenous Domain and the
Polypeptide Chain Encoded by
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Best Local S
Matches 4
                                                                                         Query Match 31.0%;
Best Local Similarity 37.9%;
Matches 39; Conservative
                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application PC/TUS9608081
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                                       117
409 TGPI-WLNEVFCFGRESSIEECKIROWGTRACSHSEDAGVTCT
                                                    350 VRLVGGSGPHEGRVEILHSGQWGTICDDRWEVRVGQVVCRSLGYPGVQAVHKAAHF-GQG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 IPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217
                                                                                                                                                                                                                     TELEFAX: (610) 270-509
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                     VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGG-KGIAKQTPFSGLG 175
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STRANDEDNESS: Single
TOPOLOGY: Linear
NCE 518 AA; 52730 MW; 1281000 CN;
                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
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CITY: King of Prussia
STATE: Pennsylvania
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                                                                                                                                                                                                                                                                                                     NAME:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                           LE TYPE: protein
451 AA; 49762 MW; 1024670 CN;
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                                                                                       Score 237; DB 3;
Pred. No. 9.70e-15;
17; Mismatches 43
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709 Swedeland Road
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APPLICANT:
                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 451 AA; 49762 MW; 1024670 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brawner, Mary TITLE OF INVENTION: Attac NUMBER OF SEQUENCES: 4
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                                                                                                                    LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217
                                                                                                                                                                                                                                                                                              LENGTH: 451 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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AL INFORMATION:
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No. 5683903
  Application US/08948222
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Elshourbagy, Nabil A.
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ID NO: 2:
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Pred. No. 9.70e-15;
17; Mismatches 43
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                                            Sequence 2, Application Patent No. 5919636 GENERAL INFORMATION:
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GENERAL INFORMATION:
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Local Similarity 37.9%;
les 39; Conservation
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                     APPLICANT:
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NAME: Jervis, Herbert H.
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Brawner, TITLE OF INVENTION: NUMBER OF SEQUENCES:
 APPLICANT: Brawner, TITLE OF INVENTION:
             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FINCE 451 AA; 49762 MW; 1024670 CN;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acid
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CITY: King of Prussia
STATE: Pennsylvania
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                                                                                         2, Application US/08973145
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                     Lysko, Paul G.
Elshourbagy, Nabil A.
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Attachment Enhanced 293 Cells
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Pred. No. 9.70e-15;
17; Mismatches 43;
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                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                      GENERAL INFORMATION:
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mes 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (610) 270-5090 INFORMATION FOR SEQ ID-NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 451 amino acids
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                   APPLICANT: Joiner, Keith TITLE OF INVENTION: Metho TITLE OF INVENTION: Seption Seption of Sequences: 2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
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ATTORNEY/AGENT INFORMATION:
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CITY: King of Prussia
                                    ZIP:
                                                                                ADDRESSEE: Patrea L. Pabst STREET: 1100 Peachtree Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Elizabeth J. Hecht
REGISTRATION NUMBER: P-4
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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o. 5624904
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451 AA; 49762 MW; 1024670 CN;
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                                               USA
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Kreiger, Monty
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Pred. No. 9.70e-15;
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Best Local :
                                                                                                                                                            Patent No. 5510466
APPLICANT: KREIGER,
TITLE OF INVENTION:
SEQ ID
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                                                                                                                                                                                                              Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: NOMO SEE.

ORGANISM: NOMO SEE.

PUBLICATION INFORMATION:

AUTHORS: Ashkenas, et al.

JOURNAL: J. Lipid Res.
                                                                                                                                                                                                                                                                                                                                                                                                                             31.0%;
Local Similarity 37.9%;
es 39; Conservetion
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
        APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 391,486
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: 272,002
FILING DATE: 15-NOV-1988
                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: YES ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (404)-815-6508
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 NO:4:
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                                                                                                                                                                                                             5510466
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451 AA; 49841 MW; 1025052 CN;
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SEQUENCE

491 AA;

54317 MW; 1350575 CN;

LENGTH: 453

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                                  SEQUENCE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/961,404
FILING DATE: 15-OCT-1992
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                 MOLECULE TYPE:
JENCE 585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
NUMBER OF SEQUENCES: 11
                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Dolo
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CITY: F
                                                      STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                 (510) 658-5470
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                                                       linear
                                                                                                                                           (510) 420-3152
                                protein
65330 MW; 1874129 CN;
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 28.7%;
35.9%;
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 Score 219; DB 2;
Pred. No. 6.96e-13;
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Pred. No. 2.13e-13;
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24 MRLADGGATNQGRVEIFYRGQWGTVCDNLWDLTDASVVCRALGFENATQALGRAAF-GQG 82

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RESULT
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Query Match
Best Local Similarity
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                                                     SEQUENCE
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                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                   MOLECULE TYPE: protein
JENCE 585 AA; 65330 MW; 1874129 CN;
                                                                                                                                                                                                                    APPLICATION NUMBER: US/0
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-19
                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
                                                                                                                                                                                                                                                                             CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Alice M.
APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                               TELEPHONE: (510) 4. TELEFAX: (510) 658-5470
                                                                                                                                                                                     NAME: Goldman, Kenneth M. REGISTRATION NUMBER: 34,174 REFERENCE/DOCKET NUMBER: 25
                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                           TOPOLOGY:
                                                                                    STRANDEDNESS:
                                                                                                 TYPE:
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                                                                                               amino acid
          Conservative
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1400 Fifty-Third Street
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                                                                           linear
                                                                                                                                                                 (510) 420-3152
                   28.7%;
35.9%;
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15-OCT-1992
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         Pred.
21; M
                    Score 219; DB 1;
Pred. No. 6.96e-13;
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          Mismatches
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          Indels
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83 SGPIMLDEVQCTGTEASLADC-KSLGWLKSNCRHERDAGVVCT 124

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117 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIA-KQTPFSGLG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5736340
GENERAL INFORMATION:
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             Local
                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 585 amino acid
                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
UENCE 585 AA; 65330 MW; 1874129 CN;
                                                                                                                                                                                                                 NAME: Goldman, Kenneth M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 2595.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 420-3152
TELEPHONE: (510) 420-3152
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,791
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                             FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
NUMBER OF SEQUENCES: 11
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                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                Similarity 35.9% 37; Conservative
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                                               Score 219; DB 1;
Pred. No. 6.96e-13;
21; Mismatches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08794795
 117
          399 VRIVGSSNR--GRAEVYYSGTWGTICDDEWQNSDAIVFCRMLGYS-KGRALYKVGAGTG- 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08794795 Patent No. 5916766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 LIPIYWSNVRCRGDEENILLCEKDI-WQGGVCPQKMAAAVTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                  y Match 28.4%;
Local Similarity 41.2%;
                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 495 amino acid
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: ATG5:
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                            MOLECULE TYPE:
                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for I
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGL 176
                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                        NAME: Han, William T
REGISTRATION NUMBER: 34,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 04-FEE
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                         42;
                                                                                LE TYPE: peptide
495 AA; 49764 MW; 1218428 CN;
                                                                                                                                                                                                                                                                                                                                                                          19406
                                         Conservative
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                                                                                                                                 495 amino acids
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04-FEB-1997

ON: 435
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                                         15;
                                                  Score 217; DB 2;
Pred. No. 1.12e-12;
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                                         Mismatches
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                                                             Length 495
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                                         Indels
                                        Gaps
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455 -QI-WLDNVQCRGTESTLWSCTKNSWGHHDCSHEEDAGVECS 494

IPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS

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Best Local :
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                                  US-08-470-350B-2
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                                                                            177 IPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217
                                                                                                  480 -QI-WLDNVQCRGTESTLWSCTKNSWGHHDCSHEEDAGVECS 519
                                                                                                                        117 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGL 176
                                                                                                                                     424 VRIVGSSNR--GRAEVYYSGTWGTICDDEWONSDAIVFCRMLGYS-KGRALYKVGAGTG- 479
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FILING DAIL.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: ATG50009P
ADPLICATION:
TOWATION:
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                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 520 AA; 52658 MW; 1340662 CN;
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: ATTELECOMMUNICATION INFORMATION TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,795
FILING DATE: 04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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Han, William T
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Pred. No. 1.12e-12;
15; Mismatches 38
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                                 1290 AA
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                                                                                                                                           Sequence 2, Application US/08200900A
                                                                                                                                                                                                            XXXXXX
                                                                                                                                                                                                                                            US-08-200-900A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08470350B
                                                                                            Sequence 2, Application US/08200900A Patent No. 5665566
                                                                                                                                                                                                                                                                                                        176 LIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                                                                                                                                                                                                                                                                                                                                                                      117 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLG-GKGIAKQTPFSGLG 175
                                                                                                                                                                                                                                                                                                                                                                                                      145 VRLVNGGDRCRGRVEILYQGSWGTVCDDSWDINDANVVCRQLGCGWALSAPGSAQF-GQG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5684126
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      204 SGSIVLDDVACRGHEAYLWSCSHRGWLSHNCGHQEDAGVICS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2,
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                                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Snyder, So
TITLE OF INVENTION: E
TITLE OF INVENTION: P
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APPLICANT:
               NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33,568
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,350B
                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1290 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Wolffe, Susan A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                             APPLICANT:
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COMPUTER: II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wolffe, Susan A REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LE TYPE: protein
1290 AA; 141879 MW; 9315616 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1290 amino acids
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1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Genetics Institute,
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Solomon H
Ebnerin: A Secreted von Ebner's Gland
Protein Associated with Taste Buds
                                              CLONING OF ENTEROKINASE AND METHOD OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches 46; Indels
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Inc.

    Legal Affairs

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Search completed: Mon Mar 13 10:26:11 2000 Job time: 8 secs.
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CC CMEDIUM TYPE: Floppy disk
CC CMEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CD OPERATING SYSTEM: PC-DOS/MS-DOS
CC CURRENT APPLICATION DATA:
CC CURRENT APPLICATION NUMBER: US/08/200,900A
CC FILING DATE: 23-FEB-1994
CC CAPPLICATION NUMBER: US/08/200,900A
CC CRECISTRATION NUMBER: GI 5201-FWC
CC REGISTRATION NUMBER: GI 5201-FWC
CT REFERENCE/DOCKET NUMBER: GI 5201-FWC
CT REFERENCE/DOCKET NUMBER: GI 5201-FWC
CC REFERENCE/DOCKET NUMBER: GI 5201-FWC
CT REFERENCE/DOCKET NUMBER: GI 5201-FWC
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Best Local Similarity 28.6%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                       457 VRLFNGTTDSSGLVQFRIQSIWHVACAENWTTQISDDVCQLLGLG-TGNSSVPTFS 511
                                                                                                                                                                                                 STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                              Score 113; DB 1; Length 798; pred. No. 1.93e-02; 10; Mismatches 29; Indels
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

dd"t protein - protein database search, using Smith-Waterman algorithm

Mon Mar 13 10:24:02 2000; MasPar time 6.39 Seconds 472.013 Million cell updates/sec

Tabular output not generated.

Title:
Description:
Perfect Score:
Sequence: >US-09-147-947-6
(117-217) from US09147947A.pep (3 of 6)
764
1 VRLRGGKNEFEGTVEVYASG.....KDIWQGGVCPQKMAAAVTCS 101

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 __1:swissprot

Statistics: Mean 38.635; Variance 55.528; scale 0.696

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	764	100.0	875	1	NETR_HUMAN	NEUROTRYPSIN PRECURSOR	1.53e-182
N	323	42.3	761	L	NETR_MOUSE	NEUROTRYPSIN PRECURSOR	.23e-
ω	256	33.5	454	ר	MSRE_RABIT	MACROPHAGE SCAVENGER R	4
4	244	31.9	458	μ	MSRE_MOUSE	MACROPHAGE SCAVENGER R	.40e-3
ر ن	237	31.0	451	<u>_</u>	MSRE_HUMAN	MACROPHAGE SCAVENGER R	2.10e-36
σ	236	30.9	1436	H	WC11_BOVIN	ANTIGEN WC1.1.	.78e-3
7	233	30.5	453	۲	MSRE_BOVIN	MACROPHAGE SCAVENGER R	.19e-3
σ	193	25.3	532	۳	SPER_STRPU	EGG PEPTIDE SPERACT RE	N
9	188	24.6	468	Н	CD6_HUMAN	T-CELL DIFFERENTIATION	3.52e-24
10	114	14.9	1069	Ь	ENTK_MOUSE	ENTEROPEPTIDASE (EC 3.	
11	113	14.8	1035	Н	ENTK_BOVIN	ENTEROPEPTIDASE PRECUR	3.64e-07
12	107	14.0	1034	ب	ENTK_PIG	ENTEROPEPTIDASE PRECUR	5.93e-06
13	105	13.7	1019	μ.	ENTK_HUMAN	ENTEROPEPTIDASE PRECUR	
14	102	13.4	583	_	CFAI_HUMAN	COMPLEMENT FACTOR I PR	5.71e-05
15	98	12.8	495	بر	CD5_BOVIN	T-CELL SURFACE GLYCOPR	'n
16	91	11.9	494	ب	CD5_MOUSE	T-CELL SURFACE GLYCOPR	6.71e-03
17	90	11.8	326	۲	PEL_EMENI	PECTATE LYASE PRECURSO	
18	88	11.5	3110	H	LMA2_HUMAN	LAMININ ALPHA-2 CHAIN	2.32e-02
19	87	11.4	491	Н	HMCS_YEAST	HYDROXYMETHYLGLUTARYL-	3.49e-02
20	84	11.0	495	<u> </u>	CD5_HUMAN	T-CELL SURFACE GLYCOPR	1.16e-01
21	83	10.9	558	_	TF65_CHICK	TRANSCRIPTION FACTOR P	1.73e-01
22	81	10.6	1857	ب	FAS2_PENPA	FATTY ACID SYNTHASE, S	3.76e-01
23	80	10.5	204	_	LEF2_NPVOP	LATE EXPRESSION FACTOR	5.52e-01

45	44	43	42	41	40	39	38	37	36	35 5	34	ω	32	31	30	29	28	27	26	25	24	
74	74	74	74	74	75	75	75	75	76	76	76	76	76	76	77	77	77	78	78	79	80	,
9.7	9.7	9.7	9.7	9.7	9.8	9.8	9.8	9.8	9.9	9.9	9.9	9.9	9.9	9.9	10.1	10.1	10.1	10.2	10.2	10.3	10.5	
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EFB3_HUMAN	EFB3_MOUSE	LUM_RAT	ID1_MOUSE	MTCY_LEUME	SOS2_HUMAN	YKZ8 CAEEL	Y96D_MYCPN	NARG_HUMAN	BACC_BACLI	HMCM_PIG	ATNB_BUFMA	CYSQ_MYCLE	ID1_RAT	RUXX_ARCFU	SOS2_MOUSE	AHPC_ECOLI	AHPC_SALTY	SNF1_SCHPO	CD5_RAT	MUC_CHICK	HEX_ADEB3	
EPHRIN-B3 PRECURSOR (E	EPHRIN-B3 PRECURSOR.	LUMICAN PRECURSOR (LUM	DNA-BINDING PROTEIN IN	BACTERIOCIN MESENTERIC	SON OF SEVENLESS PROTE	HYPOTHETICAL 143.2 KD	HYPOTHETICAL PROTEIN M	GPI-LINKED NAD(P)(+)	BACITRACIN SYNTHETASE	HYDROXYMETHYLGLUTARYL-	SODIUM/POTASSIUM-TRANS	CYSQ PROTEIN HOMOLOG.	DNA-BINDING PROTEIN IN	PUTATIVE SNRNP SM-LIKE	SON OF SEVENLESS PROTE	ALKYL HYDROPEROXIDE RE	ALKYL HYDROPEROXIDE RE	SNF1-LIKE PROTEIN KINA	T-CELL SURFACE GLYCOPR	IG MU CHAIN C REGION.	HEXON PROTEIN (LATE PR	
	5.09e+00	5.09e+00	5.09e+00	5.09e+00	3.55e+00	3.55e+00	3.55e+00	3.55e+00	2.47e+00	2.47e+00	2.47e+00	2.47e+00	2.47e+00	2.47e÷00	1.71e+00	1.71e+00	1.71e+00	1.18e+00	1.18e+00	8.08e-01	5.52e-01	

ALIGNMENTS

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(0 ·· ·· · C)	This SWISS-PR between the the European use by non- modified and entities requ or send an en	SEQUENCE FROM N TISSUB-BRAIN; MEDLINE; 982017/ PROBA K., GSCHWI "Cloning and see Biochim. Biophys -i- FUNCTION: pi ACTION MAY SI LEARNING ANI -i- SUBCELLULAR -i- SUBCELLULAR -i- SUBCELLULAR -i- SUBLEARITY: -i- SIMILARITY: -i- SIMILARITY: -i- SIMILARITY:	RESULT 1 ID NETR_HUMAN STAN AC P56730; AC p56730; DT 15-DEC-1999 (Rel. 3 DE 10-DEC-1999 (Re
CA 4; 0; ne	This SWISS-PROT entry is copyr between the Swiss Institute on the European Bioinformatics In use by non-profit institution modified and this statement is entities requires a license agor send an email to license@is.	ENCE FROM N.A. UE-BRAIN; INE; 98201705. A K., GSCHWEND T.P., SONDEREGG ning and sequencing of the cDN him. Biophys. Acta 1396:143-14 FUNCTION: PLAYS A ROLE IN NEUR FUNCTION MAY SUBSERVE STRUCTURAL LEARRING AND MEMORY OPERATIONS SUBCELLULAR LOCATION: SECRETED SIMILARITY: BELONGS TO PEPTIDA TRYPSIN FAMILY. SIMILARITY: CONTAINS 1 KRINGLE SIMILARITY: CONTAINS 4 SRCR DO.	STANI (Rel. 3) (Rel. 3) (Rel. 3) (PRECUR: (Human letazoa; imates;
ER; 1. ECEPTOR; Glycopic POTENTI NEUROTE PROLINE KRINGLE KRINGLE SRCR 1. SRCR 2. SRCR 3.	cop tute ics titu ent nse nse	SONDEREGGI of the cDN 396:143-14 396:143-14 CE IN NEUR STRUCTURAL OPERATIONS TO PEPTIDA' TO PEPTIDA' TO RETTED TO RETTED TO RETTED TO RETTED TO RETTED TO RETTED	DARD; PRT; 875 AA. 9, Created) 9, Last sequence update) 9, Last annotation update 50R (EC 3.4.21) (MOTOPS 10. Chordata; Craniata; Vert Catarrhini; Hominidae; H
3. tein; Kringle; AL. YPSIN. RICH.	yright. It is produced of Bioinformatics and Institute. There are itions as long as its is not removed. Usage agreement (See http://isb-sib.ch).	ER P.; A encoding human neurotryps (1998) REAL PLASTICITY AND THE PROPERTY REAL PLASTICITY AND THE PROPERTY REAL PLASTICITY AND THE PROPERTY REAL PLASTICITY (BY SIMILARITY). SE FAMILY S1; ALSO KNOWN AS DOMAIN. AAINS.	update) update) n update) (MOTOPSIN). (ta; Vertebrata; nidae; Homo.
Repeat;	duced through a colla s and the EMBL outs are no restrictions its content is in Usage by and for co tp://www.isb-sib.ch/a	human neurotrypsin."; ICITY AND THE PROTEOLY ATIONS ASSOCIATED WITH ARITY).	ıta; Mammalia
Signal.	produced through a collaboration thics and the EMBL outstation ties ere are no restrictions on its as its content is in no way Usage by and for commercial http://www.isb-sib.ch/announce/	CYPSIN."; PROTEDLYTIC ATED WITH N AS THE	**

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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRSS12.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Metazoa; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NETR_MOUSE STANDARD: PRT: 761 AA 008762: 05-DEC-1999 (Rel. 39, Created) 15-DEC-1999 (Rel. 39, Last sequence update) 15-DEC-1999 (Rel. 39, Last annotation updat NEUROTRYPSIN PRECURSOR (EC 3.4.21.-) (MOTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                  GSCHWEND T.P., KRUEGER "Neurotrypsin, a novel nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                           Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 98008848.
                                                                                                                                                                                                                                                                                                                                                         Mol.
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97401523.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                 AMAGUCHI N.;
Molecular cloning of a novel brain-specific
pringle-like structure and three scavenger re
                                                                                                                                                                                                                                                                                                                                                                                                                       FISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGL 229
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                                                                                                             SIMILARITY: CONTAINS 1 KRINGLE DOMAIN. SIMILARITY: CONTAINS 3 SRCR DOMAINS.
                                                                                                                                                    SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO
                                                                                                                                                                                       FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH LEARNING AND MEMORY OPERACTIONS.
TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL CORTEX, HIPPOCAMPUS
                                                                                                                                                                              AND AMYGDALA.
                                                                                                                                        TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTFFSGLGL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
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101; Conser
                                                                                                                                                                                                                                                                                                                                                         Neurosci.
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875
630
631
676
726
726
750
26
683
97011
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                                                                                                                                                                                                                                                                                                                                                                               S.R., KOZLOV S.V., multidomain serine
                                                                                                                                                                                                                                         Commun.
                                                                                                                                                 SECRETED.
O PEPTIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation update)
3.4.21.-) (MOTOPSIN)
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SERINE PROTEASE.
ZYMOGEN ACTIVATION REGION.
REACTIVE BOND (POTENTIAL).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
POTENTIAL.
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Pred. No. 1.
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1.53e-182;
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ae; Murinae;
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                                                                                                                                                                                                                                                                  ic serine receptor
                                                                                                                                                    S1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                 expressed
                                                                                                                                                                                                                                                                  protease with cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                    KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                             SONDEREGGER P.;
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Matches 4
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Q05585;
Q1-OCT-1996 (Rel. 34, Created)
Q1-OCT-1996 (Rel. 34, Last sequence up)
Q1-OCT-1996 (Rel. 34, Last annotation)
MACROPHAGE SCAVENGER RECEPTOR TYPES I
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SEQUENCE
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DISULFID
"Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger receptors.";
J. Biol. Chem. 268:2126-2133 (1923).
-i-FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS.
TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00089; trypsin; 1.
PFAM; PF00089; trypsin; 1.
DBOSTTE: PS00134; TRYPSIN_HIS;
                                                                          DOI T., WADA Y., KODAMA T., HIGASHI K.I., KURIHAR
MIYAZAKI T., NAKAMURA H., UESUGI S., IMANISHI T.,
ITAKURA H., YAZAKI Y., MATSUMOTO A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y13192; CAA73646.1;
EMBL; D89871; BAA23986.1;
MGD; MGI:1100881; PRSS12.
                                                                                                  SEQUENCE FROM N.A. MEDLINE; 93131972.
                                                                                                                                                               scavenger
                                                                                                                                                                          BICKEL P.E., FI
"Rabbit aortic
                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                     Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00134;
PROSITE; PS00135;
PROSITE; PS00420;
                                                                                                                                                      cells
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                        LDL RECEPTOR I AND II).
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                                                                                                                                                                                                                                                                                                                                                                                                                            117
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                                                                                                                                           Clin.
                                                                                                                                                                                                                                                                                                                                                                                                                                       IRLVGGNSGHEGRVELYHAGQWGTICDDQWDNADADVICRQLGLSGIAKAWHQAHF-GEG
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                                                                                                                                                                                                                                                                                                                                                                                                     SGPILLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSC
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                                                                                                                                           Invest.
                                                                                                                                                                                              93016877
                                                                                                                                                               ortic smooth muscle receptor messenger
                                                                                                                                                                                                                                          Metazoa;
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Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                    FREEMAN M.W.;
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SPERACT_RECEPTOR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.3%;
                                                                                                                                                                                                                               Leporidae;
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Pred. No. 6.23e-59;
19; Mismatches 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRINGLE.
SRCR 1.
SRCR 2.
SRCR 3.
                                                                                                                                                               cells express inducible macrophage RNA that is absent from endothelial
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
POTENTIAL.
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3F3C4F35
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ZYMOGEN ACTIVATION REGION
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                                                                                                  KURIHARA Y.
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                                                                                                                                                                                                                                                                                   (MACROPHAGE ACETYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 761;
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Query Match
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II
LDL RECEPTOR I AND II).
                                                                                                                                                                                                                                                                                                                     CARBOHYD
VARSPLIC
VARSPLIC
CONFLICT
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
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PFAM; PF01391; Collagen; 1.
Transmembrane; Glycoprotein;
Heptad repeat pattern; Recept
                                                                                                                                        MSRE_MOUSE
P30204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L11693; AAA31402.1; -.
EMBL; L11692; AAA31403.1; -.
EMBL; D1381; BAA02649.1; -.
PROSITE; PS00420; SPERACT_RECEPTOR;
        SEQUENCE FROM N.A.
MEDLINE; 93359822.
ASHKENAS J., PENMAN
                                                Eutheria;
                                                          Eukaryota;
                                                                     Mus musculus (Mouse)
                                                                              MSR1 OR SCVR.
                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                        176
                                                                                                                                                                                                                                                353 VRLVGGRGPHEGRVEILHNGQWGTVCDDHWELRAGQVVCRSLGYRGVKSVHKKAYF-GQG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODIFIED LOW DENSITY LIPOPROTEINS (LDL)
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE
ALTERNATIVE PRODUCTS: THE TWO FORMS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        읁
                                                                                                                                                                                       LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                                                                                                                                                                                                         TGPI-WLNEVPCLGMESSIEECKIRQWGVRVCSHGEDAGVTCT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR
                                                                                                                                                                                                                            VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQL-GGKGIAKQTPFSGLG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE SAME GENE.
  Ζ.
                                                                                                                                                                                                                                                                               Similarity
                                                 ; Metazoa;
Rodentia;
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                                                                                                                                                 STANDARD;
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                                               Chordata; Craniata; Ve. Sciurognathi; Muridae;
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73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor; Alternative splicing.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
           VASILE
                                                                                                                                                                                                                                                                                                           WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE II MEMBRANE PROTEIN.
THE TWO FORMS OF MACROPHAGE SCAVENGER
II) ARE PRODUCED BY ALTERNATIVE SPLIC
                                                                                                                                                                                                                                                                    17;
                                                                                                                                                                                                                                                                              Score 256; DB 1;
Pred. No. 2.76e-41;
                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocytosis; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-HELICAL COILED-COIL COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPACER (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
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Bioinformatics and the EMBL outstation -
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           ACTON
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                                                         Vertebrata;
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                                                                                                                                                AΑ
                                                  Murinae;
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                                                                                                (MACROPHAGE ACETYLATED
           FREEMAN M.W
                                                                                                                                                                                                                                                                                       Length 454;
                                                                                                                                                                                                                                                                    Indels
                                                 Mammalia;
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EMBL; L04274; AAA39747.1; ALT_INIT.
EMBL; L04275; AAA39748.1; ALT_INIT.
EMBL; D13382; BAA02650.1; -
EMBL; M59445; AAA37464.1; -
EMBL; M59445; AAA37465.1; -
EMBL; U3943; AAC13774.1; -
EMBL; U3873; AAC13774.1; -
PIR; A38260; A38260.
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                    CARBOHYD
CARBOHYD
                                                           DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Lipid Res. 36:1305-1314(1995)
-!- FUNCTION: MEMBRANE GIXCOPPOTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENES TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE ENDOCYTOSIS OF A DIVERSE GROUP OF MACRONECULES, INCLUDING MODIFIED LOW DENSITY LIPOPROTEINS (LDL).
-!- SUBUNIT: HOMOTRIMER.
-!- SUBUNIT: HOMOTRIMER.
-!- SUBUNIT: HOMOTRIMER.
-!- ALTERNATIVE PRODUCTS: THE TWO FORMS OF MACROPHAGE SCAYENGER RECEPTOR (TYPES I AND II) ARE PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                      Heptad
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFTRING R.P., FREEMAN M.W.;
AFTRING R.P., FREEMAN M.W.;
"Structure of the murine macrophage scavenger receptor gene and
evaluation of sequences that regulate expression in the macrophage
cell line, P38BD.";
cell line, P38BD.";
                                                                                                                                                                                                                                                                           MGD: MGI:98257; SCVR.
PROSITE; PS00420; SPERACT_RECEPTOR;
PFAM; PF00530; SRCR; 1.
PFAM; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIYAZAKI T., NAKAMURA H., UESUGI S.,
ITAKURA H., YAZAKI Y., MATSUMOTO A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (SHORT FORM). MEDLINE; 93131972.
                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "An ancient, highly conserevealed by cloning type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JENKINS N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              charged macromolecules by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structures and high and low affinity ligand binding properties murine type I and type II macrophage scavenger receptors."; J. Lipid Res. 34:983-1000(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-4 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FREEMAN M., ASHKENAS J., REES
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pend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by non-profit institutions as long fied and this statement is not removed
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NAKAMURA H., UESUGI S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  highly conserved
                                                                                                                                                                                                                                    pattern;
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78
                                                                                                                                                                                           otein; Endocytosis; Coiled coil; LDL;
Receptor; Alternative splicing.
CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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POTENTIAL.
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POTENTIAL.
                                                                                CYS-RICH.
                                                                                                COLLAGEN-LIKE
                                                                                                                   SPACER (PROBABLE).
ALPHA-HELICAL COILED-COIL
                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87:8810-8814(1990).
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, IMANISHI T., 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the recognition of negatively scavenger receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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KAWABE
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ATHEROGENESIS.
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CARBOHYD
VARSPLIC
VARSPLIC
SEQUENCE
PFAM; PF00530; SRCR; 1.

PFAM; PF01391; Collagen; 1.

Transmembrane; Glycoprotein; Endocytosis; Coiled coil; LDL;

Heptad repeat pattern; Receptor; Alternative splicing.

DOMAIN 1 50 CYTOPLASMIC (POTENTIAL).

TRANSMEM 51 76 SIGNAL-ANCHOR (TYPE-II MEMBRANE DOMAIN 77 451 EXTRACELLULAR (POTENTIAL).
                                                                                                                                EMBL; D90187; BAA14208.1;
EMBL; D90188; BAA14209.1;
PIR; A38415; A38415.
PIR; B38415; B38415.
MIM; 153622; -
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                       and localization in atherosclerotic lesions.";

Proc. Natl. Acad. Sci. U.S.A. 87:9133-9137(1990).

-:- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS. TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING MODIFIED LOW DENSITY LIPOPROTEINS (LDL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASRE_HUMAN STANDARD: PRT; 451 AA.
P21757; P21759;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II (MACROPHAGE ACETYLATED
                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                  PROSITE; PS00420; SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATSUMOTO A., NAITO M., ITAKURA H., IKEMOTO S., ASAOKA H., HAYAKAWA I., KANAMORI H., BURATANI H., TAKAKU F., SUJUKI H., KOBARI Y., MIYAI T., TAKAHASHI K., COHEN E.H., WYDRO R., HOUSMAN D.E., KODAMA T.;
"Human macrophage scavenger receptors: primary structure, expression,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
RECEPTOR (TYPES I AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR I AND II).
                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                              OF THE SAME GENE.
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                                                                                                                                                                                                                                                                                                                                                                            TYPE II MEMBRANE PROTEIN.
THE TWO FORMS OF MACROPHAGE SCAVENGER
II) ARE PRODUCED BY ALTERNATIVE SPLIC
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No. 3.40e-38;
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01-APR-1993
01-FEB-1994
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PIR; S19913; S19913.
PIR; A46496; A46496.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTIGEN WC1
Bos taurus
                                                                                              PFAM; PF00530; SRCR;
Antigen; Repeat.
                                                                                                                                   PROSITE; PS00420;
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                                                                                                                                                                                                             s requires a license agreement (S an email to license@isb-sib.ch).
   Similarity 39; Conser
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39; Conser
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Pred. No. 2.
17; Mismatc
Score 236; DB 1;
Pred. No. 3.78e-36;
20; Mismatches 40
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ALPHA-HELICAL COII
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.10e-36;
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Pecora; Bovoidea; Bovi
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1155 LRLRGGDSECSGRVEVWHNGSWGTVCDDSWSLAEAEVVCQQLGCGQALEAVRSAAF-GPG 1213

117 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLG-GKGIAKQTPFSGLG 175

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EMBL; X54183; CAA38108.1; -.
PIR; S08276; S08276.
PIR; S08278; S08278.
PROSITE; PS00420; SPERACT_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Type I macrophage scavenger collagen-like coiled coils."; Nature 343:531-535(1990).
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                                                                                                                                PFAM; PF00530; SRCR; 1.
PFAM; PF01391; Collagen; 1.
Transmembrane; Glycoprotein; Endocytosis; Colled coil; LDL;
                                                                                                                                                                                                                                                      Asse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos.
[1]
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01-MAY-1991 (Rel. 18, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II (MACROPHAGE ACETYLATED
                                    DOMAIN
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KODAMA T., FREEMAN M.,
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                                                                                   Receptor: Alternative splicing.
CTTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
EXTRACELLULAR (POTENTIAL).
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        POTENTIAL.
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                                    COLLAGEN-LIKE.
CYS-RICH.
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BY ALTERNATIVE SPLICING
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Proc. Natl. Acad. Sci. U.S.A. 86:2128-2132(1989).
-!- FUNCTION: RECEPTOR FOR THE EGG PEPTIDE SPERACT.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPER_STRPU STANDARD: PRT: 53
P16264;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence upd
15-JUL-1999 (Rel. 38, Last annotation u
EGG PEPTIDE SPERACT RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                            Receptor;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
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Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
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  Similarity 38; Conser
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25.3%;
llarity 35.8%;
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                                                                                        WW;
Score 193; DB 1;
Pred. No. 2.13e-25;
19; Mismatches 41
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ein that crosslinks
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                                        Length 532;
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P30203;
01-APR-1993 (Rel. 25, Created)
01-APR-993 (Rel. 25, Last seq)
15-DEC-1998 (Rel. 37, Last ann
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ukaryota; Metazoa; Chordata; Craniata; Vertebrata;
utheria; Primates; Catarrhini; Hominidae; Homo.
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$26741; $26741.
186720; -.
GRMYYS---CNGEELTLSNCSWRFNNSNLCSQSLAARVLCS 361
                                                      RLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFS-GLGL 176
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                                                                                                         RLTGGADRCEGQVEVHFRGVWNTVCDSEWYPSEAKVLCQSLG-CGTAVERPKGLPHSLS- 323
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Similarity 36.6%;
37; Conservative
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N ANTIGEN CD6 PRECURSO
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                                                                                                                                                                  19;
                                                                                                                                                                                         Score 188; DB 1;
Pred. No. 3.52e-24;
                                                                                                                                                                                                                                                                            POTENTIAL.
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P97435;
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PF01390; SEA; 1.
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Zymogen; 829 1069 47 268 379 549 679

NON-CATALYTIC CHAIN (HEAVY CHAIN).
CATALYTIC CHAIN (LIGHT CHAIN).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LDL-RECEPTOR CLASS A 1.
CUB.
MAM.
CUB.

Transmembrane;

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MGD; MGI:1197523; PRSS7.

PROSITE; PSO0134; TRYPSIN_HIS; 1
PROSITE; PSO0135; TRYPSIN_SER; 1
PROSITE; PSO01180; CUB; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
PROSITE; PS50060; MAM_2; 1.
PROSITE; PS50068; LDLRA_2; 2.
PROSITE; PS01209; LDLRA_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YUAN X., LU D., RUBIN D.C., PUNG C.Y.M., SADLER J.E.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC
PROTEOLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE
A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN
TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN,
PROCARBOXYPEPTIDASES, AND PROELASTASES (BY STMILARITY).
-i- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                     EMBL; U73378; AAB37317.1; HSSP; P00763; 1DPO.
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Mus musculus (Mouse).
Riikarvota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUL-1998 (Rel.
PFAM; PF00057; ldl_recept_a;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYM: THE CHAINS ARE DEWLVED FROM A SINGLE PRECURSOR THAT I CLEAVED BY A TRYPSIN-LIKE PROTEASE (BY SIMILARITY).

SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.

SIMILARITY: CONTAINS 2 CUB DOMAINS.

SIMILARITY: CONTAINS 1 SRCR DOMAIN.

SIMILARITY: CONTAINS 1 SRCR DOMAIN.

SIMILARITY: CONTAINS 1 MAM DOMAIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HETERODIMER OF A CATALYTIC (LIGHT) CHAIN AND MULTIDOMAIN (HEAVY) CHAIN LINKED BY A DISULFIDE BOND (
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6, Last annotation updat
3.4.21.9) (ENTEROKINASE
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01-FEB-1996
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J. Biol.
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               SEQUENCE OF 801-1035 FROM N.A., AND PARTIZ MEDITOR; 94043122.

LAVALLIE E.R., REHEMTULLA A., RACIE L.A., FERENZ C., GRANT K.L., LIGHT A., MCCOY J.P.

"Cloning and functional expression of a closubunit of bovine enterokinase."

J. Biol. Chem. 268:23311-23317(1993).
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                                                                                                                                  KilaMoTO Y., YUAN X., WU Q., MCCOURT D.W., SADLER J.E.; "Enterokinase, the initiator of intestinal digestion, is protease composed of adstinctive assortment of domains. Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
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Eukaryota; Metazoa;
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KILAMOTO Y., YUAN
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16; Conser
                                                                                                                                                                                                                                                                    Cetartiodactyla;
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(Rel. 33, Last sequence update)
(Rel. 39, Last annotation update)
ASE PRECURSOR (EC 3.4.21.9) (ENTEROKINASE)
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SRCR.
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d. No. 2.27e-07;
Mismatches 25;
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A). IT CATALYZES THE CONVERSION OF TRYPSIN OF TRYPSIN WHICH IN
TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN,
PROCARBOXYPEPTIDASES, AND PROELASTASES.
-! CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
TRYPSINOGEN.
-! SUBUNIT: HETERODIMER OF A CATALYTIC (LIGHT) CHAIN AND A
MULTIDOMAIN (HEAVY) CHAIN LINKED BY A CTETTER OF THE CHAIN AND A
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PFAM; PF00089; trypsin;
PFAM; PF00431; CUB; 2.
PFAM; PF00530; SRCR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVED BY A TRYPSIN-LIKE PROTEASE.
-!- SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLAS-
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: CONTAINS 1 SRCR DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92189715.
LIGHT A., JANSKA H.;
"The amino-terminal
                                                                                        TIPID
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                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                              Signal-anchor;
                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MULTIDOMAIN (HEAVY) CHAIN LINKED BY A DISULFIDE BOND. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE) TISSUE SPECIFICITY: INTESTINAL BRUSH BORDER. PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT
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MAM_1; 1.

MAM_2; 1.

LDLRA_1; 2.

LDLRA_2; 2.
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Transmembrane; Repeat; Alternative sp
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CHARGE RELAY SYSTEM (BY CHARGE RELAY SYSTEM (BY CHARGE RELAY SYSTEM (BY MYRISTATE (POTENTIAL).
BY SIMILARITY.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LDL-RECEPTOR CLASS A 1.
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MIKI K., KUROKAWA K., TASHIRO K., SHIOKAWA K., SHINOMIYA K.,
UMEYAMA H., INOUE H., TAKAHASHI T., TAKAHASHI K.,
"Structural characterization of porcine enteropeptidase.";
J. Biol. Chem. 269:19976-19982(1994).
J. Biol. Chem. 269:19976-19982(1994).
J. FUNCTION: RESPONSIBLE FOR INTITIATING ACTIVATION OF PANCREATIC PROTEDLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE
PROTEDLYTIC PROENZYMES (TRYPSIN) OF TRYPSIN OF TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN,
PROCARBOXYPEPTIDASES, AND PROENZYMES OF 6-LYS-(-ILE-7 BOND IN TRYPSINOGEN, STANGER, STA
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P98074;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ENTEROPERTIDASE PRECURSOR (EC 3.4.21.9) (ENTEROKINASE)
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Eukaryota; Metazoa; Chordata; Craneutheria; Cetartiodactyla; Suina;
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SUBUNIT: HETEROTRIMER OF A CATALYTIC (LIGHT) CHAIN, A MUL: (HEAVY) CHAIN, AND A MINI CHAIN.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE)
PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT:
CLEAVED BY A TRYPSIN-LIKE PROTEASE.
PTM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.
SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
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ina; Suidae;
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                                                                                               (LIGHT) CHAIN, A MULTIDOMAIN
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  PROSITE; PS00134; TRYPSIN_HIS; 1
PROSITE; PS00135; TRYPSIN_SER; 1
PROSITE; PS01180; CUB; 2.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
PROSITE; PS01209; LDLRA_1; 2.
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Serine protease;
CHAIN 52
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0068; LDLRA_2; 2.
1dl_recept_a; 2
; trypsin; 1.
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NON-CATALYTIC M CHAIN (MINI CHAIN).
NON-CATALYTIC H CHAIN (HEAVY CHAIN).
CATALYTIC L CHAIN (LIGHT CHAIN).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LDL-RECEPTOR CLASS A 1.
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "ENTERONO Y., YUAN X., WU Q., MCCOURT D.W., SADLER J.E.;
"Enterokinase, the initiator of intestinal digestion, is a mosaic protease composed of a distinctive assortment of domains.";
Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
-!- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC PROPROMYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE A). IT CATALYZES THE CONVERSION OF TRYPSINGEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINGEN, PROCARBOXYPEPTIDASES, AND PROELASTASES.
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KITAMOTO Y., VEILE R.A., DONIS-KELLER H., SA
"CDNA sequence and chromosomal localization
the proteolytic activator of trypsinogen.";
piochemistry 34:4562-4568(1995).
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**Ol-FEB-1996 (Rel. 33, Last septence update)
**15-JUL-1998 (Rel. 36, Last annotation update)
**ENTEROPEPTIDASE PRECURSOR (EC 3.4.21.9) (ENTEROKINASE).
**PRSS7 OR ENTK.
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EMBL; U09860; AAC50138.1;
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DISEASE: DEFECTS IN PRSS7 CAUSE LIFE-THREATENING INTESTINAL MALABSORPTION CHARACTERIZED BY DIARRHEA AND FAILURE TO THRI SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.

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SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
TISSUE SPECIFICITY: INTESTINAL BRUSH BORDER.
PTM: THE CHAINS ARE DERLYED FROM A SINGLE PRECURSOR THAT II
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Pred. No. 5.93e-06;
12; Mismatches 29
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PFAM; PF00089; trypsin; 1.
PFAM; PF000431; CUB; 2.
PFAM; PF00530; SRCR; 1.
PFAM; PF00629; MAM; 1.
PFAM; PF01390; SEA; 1.
Signal-anchor; Glycoprotein; Myristate; Hydrolase;
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; LDLRA_1; 2.
; LDLRA_2; 2.
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784 NON-CATALYTIC CHAIN (HEAVY CHAIN).
1019 CATALYTIC CHAIN (LIGHT CHAIN).
47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
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28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLDBERGER G., BRUNS G.A.P., RITS M., EDGE M.D., KWIATKOWSKI D.J.;
Human complement factor I: analysis of cDNA-derived primary
structure and assignment of its gene to chromosome 4.";
J. Biol. Chem. 262:10065-10071(1987).

-i- FUNCTION: FACTOR I IS RESPONSIBLE FOR CLEAVING THE ALPHA-CHAINS
OF C4B AND C3B IN THE PRESENCE OF THE COFACTORS C4-BINDING
PROTEIN AND FACTOR H RESPECTIVELY.

-i- SUBUNIT: HETERCOIMER OF A LIGHT AND HEAVY CHAINS LINKED BY
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EMBL; J02770; AAA52455.1; -.
PIR; A29154; A29154.
HSSP; P00763; 1DPO.
SWISS-2DPAGE; P05156; HUMAN.
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13-AUG-1987 (Rel. 05, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
COMPLEMENT FACTOR I PRECURSOR (EC 3.4.21.45)
                                                                                                                                                                       DOMAIN
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DLDBERGER G., BRUNS G.A.P.,
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SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: PLASMA.
SIMILARITY: BELONGS TO PEPTIDASE FAM
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PS00135; TRYPSIN_SER;
PS01209; LDLRA_1; 1.
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Primates; Catarrhini;
      (Human).
etazoa; Chordata; Craniata; Vertebrata; Mammalia;
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COMPLEMENT FACTOR I LIGHT CHAIN.
LDL-RECEPTOR CLASS A 1.
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD5_BOVIN STANDARD; PRT; 455 AA.
P19238;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR (LYMPHOCYTE GLYCOPROTEIN T1_LEU-1) (LYMPHOCYTE ANTIGEN CD5)
                       CARBOHYD
CARBOHYD
                                                                                                                                                                                                                             Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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CONFLICT
                                                                                                                                                                    DOMAIN
TRANSMEM
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ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence of bovine CD5.";
"Sequence of bovine CD5.";
Nucleic Acids Res. 18:5296-5296(1990).
-!- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING PROLIFERATION. CD5 INTERACTS WITH CD72/LYB-2.
-!- SUBCELULAR LOCATION: WYPE I MEMBRANE PROTEIN.
-!- SUBCILIULAR LOCATION: 3 SECR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                               DOMAIN
                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                              EMBL; X53061; CAA37231.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                        PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 LGLIPIYWSNVRCRGDEENILLC 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 VSLKHGNTDSEGIVEVKLVDQDKTMFICKSSWSMREANVACLDLGFQQGADTQRRFKLSD 173
                                                                                                                                                                                                                                                                                         S11270;
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Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90384847.
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                                                                                                                                                                                                                                                                        SRCR; 3
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                                                                                                                                                                                                                                                Glycoprotein; T-cell
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Pred. No. 5.71e-05;
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POTENTIAL.
V -> F (IN
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POTENTIAL.
POTENTIAL.
                                                                                                       SRCR
SRCR
                                                                                                                                               CYTOPLASMIC
                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                     T-CELL SURFACE
EXTRACELLULAR
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D673E9F0
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CRC32;
                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSTEM (BY SIMILARITY).
SYSTEM (BY SIMILARITY).
                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                        GLYCOPROTEIN CD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BURNY A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 583;
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h co ime	118	275	Query Match Best Local : Matches	SEQUENCE
Search completed: M Job time : 11 secs.	RLR	P1.V	atch cal	ENCE
secs	GGKNI	NUS DE	Simi:	4
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Search completed: Mon Mar 13 10:24:13 2000 Job time : 11 secs.	::	2000	12.8%; al Similarity 39.1%; 18; Conservative	4333
0:24	A-MG	OK E.J.	יט טי	MW;
:13	TVCS		core red. 9;]	F8.
2000	SHWDI	74837	98; No. Misma	ED2AE
		275 BIVGGSDVCFGSVFVBSGKGOKWDTICDDSWAKGTABBVFVCBFOO 320	Query Match 12.8%; Score 98; DB 1; Length 495; Best Local Similarity 39.1%; Pred. No. 3.35e-04; Matches 18; Conservative 9; Mismatches 15; Indels	495 AA; 54333 MW; F8ED2AEO CRC32;
	-V-I	DVEV	1; e-04 s 1	C32;
	CHQL	0.50	Leng	
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protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:24:29 2000; MasPar time 16.49 Seconds 424.656 Million cell updates/sec

>US-09-147-947-6 (117-217) from US09147947A.pep (3 of 6)

Description: Perfect Score:

Sequence: 1 VRLRGGKNEFEGTVEVYASG.....KDIWQGGVCPQKMAAAVTCS 101

Scoring table: РАМ 150 Gap 11

Searched:

225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

ptrembll2 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 37.758; Variance 56.548; scale 0.668

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	% Query Match	Length	DB	IJ	ripti	Pred.	No.
1	266		2153	5	097375	SCAVENGER RECEPTOR CYS	4.54e	-42
N	254	33.2	2043	თ	096943	IN, MEMBRA	. 51	
w	251		1036	ഗ	097378	SCAVENGER RECEPTOR CYS	. 51	ω
4	251	•	1116	4	Q07898	M130 ANTIGEN PRECURSOR	.51e	ů
υ	251		1149	4	Q07901	M130 ANTIGEN, EXTRACEL	. 51	۵
σı	251		1151	4	007899	O ANTIGEN,	51	ώ
7	251		1156	4	Q07900	0	.51e	۵
œ	250		754	11	Q9Z175	LYSYL OXIDASE-RELATED	. 45e	ώ
9	243	•	638	4	091518	OXIDASE-	. 41	ώ
10	243	•	774	4	Q9Y4K0	LYSYL OXIDASE-RELATED	1e	36
11	242		480	σ	Q29112	SCAVENGER-RECEPTOR PRO	'n	ω
12	242	31.7	804	σ	Q29113	SCAVENGER-RECEPTOR PRO		w
13	240	•	1785	4	Q9Y4V9	DMBT1/6KB.1 PROTEIN PR	w	ω
14	240	•	1785	4	Q9Y211	DMBT1 PROTEIN.	ω	ώ
15	239	31.3	369	σ	Q29110	SCAVENGER-RECEPTOR PRO		ώ
16	239		518	11	Q60754	BACTERIA BINDING MACRO	. 34	ώ
17	238	•	437	თ	Q29109	SCAVENGER-RECEPTOR PRO	. 12	ώ
18.	234		600	σ	Q28910	MUCIN (FRAGMENT).	. 96	ώ
19	233		1594	თ	Q95218	z	6.97e-	34
20	230	•	918	13	9	PEMA-SRCR PROTEIN PREC	. 79	ω
0	230	00.	-	1 010	T 910 13	TO CASOR	13 C92096 FEMA-SRCK PROTEIN	13 Q92090 FEMA*SRCK FROTEIN FREC 3./9

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01-MAY-1999 (TrEMBLrel. 10, Created)

US-09-147-947-6-03. rspt Nolhang behwlhun PIRE Sarisprok hits

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21	225		347	4	043866	SP ALPHA.	6.29e-32
22	219	28.7	585	4	838	()	.81e-3
23	217		483 1	\vdash	Q9WUB9	Ω	ώ
24	217		520	4	Q9Y5S3	MACROPHAGE RECEPTOR.	.51e-3
25	215		2083 1		6099		1.68e-29
26	212	27.7	356 6	σ	097682	UNKNOWN MRNA, PARTIAL	.87e-
27	212	•	574 1	Н	070513	MAMA.	.87e-2
28	212	27.7	1290 1	۳	Q62827	EBNERIN.	'n
29	211		822 13	w	Q9YHC1	LYSYL OXIDASE HOMOLOG	.54e-2
30	211		895 1	w	Q9W6N1	OXIDASE	ည်
31	210		868 5	G	Q9Y1V3	TUNICATE RETINOIC ACID	.69e-2
32	209		127	σ	Q95316		.67e-
33	206		504	σ	Q28908	MUCIN (FRAGMENT).	2.45e-27
34	205		578 11	دسو	P70117	PANCREAS CANCER-ASSOCI	.24e-
35	204		665 1	_	Q61003	T-CELL DIFFERENTIATION	.36e-
36	202	26.4	. 531 5	5	Q17064	SP85.	2.21e-26
37	202		577 1	ш	Q07797	PEPTIDYLPROLYL ISOMERA	.21e-2
38 8	198		532	G	Q25111	A SPERM-ACTIVATING PEP	1.97e-25
39	194	25.4	352 1	1	035301	SP-ALPHA.	-2
40	194		352 1	μ,	035300	SP-ALPHA.	.75e-2
41	191	٠	462	σ	Q28881	MEMBRANE PROTEIN SCAVE	.92e-
42	191		574 1	_	035649		.92e-
43	188	•	595	4	Q9Y4K9	CD6C.	4.52e-23
44	188	24.6	601	4	Q9Y4K8	CD6D.	ò
4 5	188	4.	635	4	Q9Y4L0	CD6B.	'n

ALIGNMENTS

AC	ij	RESULT	Qy	Db	Qу	DЪ	Query Best Match	SQ FT	H	FΤ	KW	DR.	尿	2 2	7 P	9 2	7 Z	2 R	RN	გ	8	გ	SO	GN	DE I	7 (3 5	3 2	3 5	RESULT	
	O96943 PRELIMINARY; PRT; 2043 AA.	2	177 IPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217	522 VPILLDNVGCSGNERSLELCSNNGIGVHNCGHQEDASVVCT 562	117 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGL 176	462 VRLVGGLNNREGRVEIFLNNQWGTVCDDDWGTPDANVVCRQLGYPSGGSARSSAYFGRGS 521	Query Match 34.8%; Score 266; DB 5; Length 2153; Best Local Similarity 38.6%; Pred. No. 4.54e-42; Matches 39; Conservative 22; Mismatches 40; Indels 0; Gaps 0;	SEQUENCE 2153 AA; 226557 MW; CA3BA8A9 CRC32;	2153	16 POTENTIAL.		PROSTTE: PS00420: SPERACT RECEPTOR: 15	EMBL; AF064259; AAD08654.1;	ຄຼ	System Expressed	the Mammalian Immune System: Itanscription rectors	1			ongylocentrotus.	Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;	; Echinodermata; Ecl	Strongylocentrotus purpuratus (Purple sea urchin).		CEPTOR CYSTEINE-RICH	(Tremaire) 12.	Last	(Trempine) 10	09/2/7. FREHEMINGEL, FRE, \$100 pm.	07375 0001 TMINADV. 000. 0153	

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 B
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Best Local
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                 "Origins of Immunity: Transcription Factors and Effector Genes Vertebrate Immune System Expressed in Sea Urchin Coelomocytes." Immunogenetics 0:0-0(1999).
EMBL; AF076513 AAD05493.1; -.
Signal; Recentra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tery Match
                                                                                                                                                                                                                         Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  097378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The putative sponge aggregation receptor. Isolation characterization of a molecule composed of scavenger cysteine-rich domains and short consensus repeats.";
J. Cell Sci. 111:2635-2644(1998).
EMBL; Y14953; CAA75175.1;
HSSP; P10998; TVVC.
PROSITE: PS00420; SPERACT_RECEPTOR; 8.
BEQUENCE 2043 AA; 220896 MW; 4CE19401 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SCAVENGER RECEPTOR CYSTEINE-RICH PROTEIN PRECUSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1319
207898
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1261 LRLVNGNTEGEGRVEVFHRGSWGTVCDDHWSEIDANIVCKELGFA-RAIS-ASGFATFGE 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLUMBACH B., PANCER Z., DIEHL-SEIFERT MUELLER I., MUELLER W.E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 98369060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRCR DOMAIN,
SRCRM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geodia cydonium (Sponge).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Astrophorida;
                                                  174
                                                                          784
                                                                                                117
                                                                                                                          725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                              VRLVGGSNEAEGRVEIOY-NGVWGTICDDSWDITDASVVCRMLGFQGASGAPGSAQFGQG 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSGTIWLDDVQCDGTEATIFNCPSSGWGNHNCLHSEDASAICT 1361
                                                               TGLIQL--DDVGCTGAEQTIFDCAHPAFGVHNCAHYEDAGVVC
                                               LGLIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IP-IYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.2%;
Similarity 34.0%;
35; Conservation
                                                                                                                                                              Similarity
                                                                                                                                                                                                 21 10
1036 AA;
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da; Geodiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.) (TrEMBLrel.
 PRELIMINARY;
                                                                                                                                                32.9%;
larity 41.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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1036
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12, Last
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                                                                                                                                                Score 251; |
Pred. No. 2.
18; Mismatc
                                                                                                                                                                                                  WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 254; DB 5;
Pred. No. 4.51e-39;
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                                                                                                                                                                                                 POTENTIAL.
SCAVENGER RECEPTOR CYSTEINE-RICH
W; CBE8C531 CRC32;
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Demospongiae;
                                                                                                                                                  Mismatches
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 1116
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                                                                                                                                                             DB 5;
.51e-38;
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                                                                                                                                                                        Length 1036;
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Best Local
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Q07901;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1999 (TrEMBLrel. 1
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01-NOV-1996 (
01-NOV-1999 (
 MEDLINE;
LAW S.A.,
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SIGNAL
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EMBL; Y18400; CAB45233
EMBL; Y18401; CAB45233
EMBL; Y18402; CAB45233
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                                                                      Eutheria;
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EMBL; Y18395; CAB45233
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EMBL; Y18388;
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Metazoa; Chordata;
                                   SEQUENCE
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RITTER M., BUECHLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scavenger receptor
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                                                                                                                                                                                                                                                                                                                            TGPI-WINEVKCKGNESSLWDCPARRWGHSECGHKEDAAVNCT
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Y18398; CAB45233
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Y18391; CAB45233
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Y18393; CAB45233
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F00530; SRCR; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                    FROM N.A. 93380506.
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 MICKLEM
                                                                        Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1116 AA;
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larity 39.8%;
Conservative
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 К.J.,
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                                                                      Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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n of the human CD163 gene.";
to the EMBL/GenBank/DDBJ databases
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16 M130 ANTIGEN.
120979 MW; F193FBBA CRC32;
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SHAW J.M.,
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18;
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Pred. No. 2.51e-38;
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 ZHANG X.P.,
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Best Local :
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Q07899;
                                                             Q07900 PRELIMINARY;
Q07900;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1999 (TrEMBLrel. 12,
M130 ANTIGEN, CYTOPLASMIC VARIANT 2 PRECURSOR Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertel
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MEDLINE; 93380506.
LAW S.A., MICKLEM K.J.,
MASON D.Y.;
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Homo sapiens (Human).

Craniata;

Craniata;

Hominid
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
M130 ANTIGEN, CYTOPLASMIC VARIANT 1 PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scavenger receptor superfamily.";
Eur. J. Immunol. 23:2320-2325(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    924 IRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQVVCQQLGCGPALKAFKEAEF-GQG
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                                                                                                                                                                                                                                                                                          983 TGPI-WLNEVKCKGNESSLWDCPARRWGHSECGHKEDAAVNCT 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z22969; CAA80542.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00258; SPERACTRCPTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
41; Conser
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1151 AA;
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larity 39.8%;
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51 M130 ANTIGEN,
124820 MW; A72EDD2F (
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                                                                    Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 251; DB 4; Le
Pred. No. 2.51e-38;
18; Mismatches 40;
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Pred. No. 2.51e-38;
18; Mismatches 40
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M130 ANTIGEN,
WW; 4901C708 C
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EMBL; AF053368; AAC83205-1; -
EMBL; AF084363; AAC95338.1; -
SEQUENCE 754 AA; 83681 MW; 6
LT 9
975Y8 PRELIMINARY; PRT; 638 AA. 09Y5Y8; PRT; 638 AA. 09Y5Y8; Created)
01-NOV-1999 (TremBLrel. 12, Last sequence up 01-NOV-1999 (TremBLrel. 12, Last annotation LYSYL OXIDASE-LIKE PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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O9Z175 PRELIMINARY; PRT; 754 AA.

O9Z175; O1-MAY-1999 (TIEMBLrel 10, Created)

O1-MAY-1999 (TIEMBLrel 11, Last sequence update)

O1-AUG-1999 (TIEMBLRel 11, Last annotation update)

O1-AUG-1999 (TIEMBLRel 11, Last annotation update)

LYSYL OXIDASE-RELATED PROTEIN 2 (LOR2 PROTEIN).
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SEQUENCE
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MEDLINE; 99126643.
JANG W., HUA A., SPILSON S.V
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                    GAIHLSEVRCSGQEPSLWRCPSKNI-TAEDCSHSQDAGVRCN
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Similarity 40.2%;
41; Conservative
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1156 AA;
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Pred. No. 4.
20; Mismatc
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M130 ANTIGEN,
2 MW; 287A07A0 C
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18; 1
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILLER W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  668B44B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              re 250; DB 11; L
d. No. 4.45e-38;
Mismatches 39;
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Best Local
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Q9Y4K0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Regulation of a Novel Gene Encoding a in Cellular Adhesion and Senescence."; J. Biol. Chem. 0:0-0(1997).
EMBL: U89942; AAB49697 1; -
PROSITE; PS00420; SPERACT_RECEPTOR; 1.
SEQUENCE 774 AA; 86724 MW; 1A5C47AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPY4KO:
O1-NOV-1999 (TEMBLrel. 12, Created)
O1-NOV-1999 (TEMBLrel. 12, Last sequence update)
O1-NOV-1999 (TEMBLrel. 12, Last annotation update)
LYSYL OXIDASE-RELATED PROTEIN.
WS9-14.
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ
EMBL; AF117949; AAD34343.1; -
PROSITE: PS00420; SPERACT_RECEPTOR; 1.
SEQUENCE 638 AA; 71101 MW; C232E6A4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SAITO H., PAPACONSTANTINOU J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa; (
Eutheria; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The LOXL2 gene encodes a new lysyl oxidase-like expressed at high levels in reproductive tissues. T. Biol. Chem. 274:12939-12944(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=SPLEEN, PLACENTA; MEDLINE; 99230328.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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JOURDAN-LE SAUX C., CSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGG-KGIAKQTPFSGLG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVSASVVCRELGFGSAKEAVTGSRL-GQG 183
                                                                                                                                                       LIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                                                                                                                                                                                                    IGPIHLNEIQCTGNEKSIIDCKFNA-ESQGCNHEEDAGVRCN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
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                                                                                                                                                                                                                                                        VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGG-KGIAKQTPFSGLG
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                                                                                                                                                                                                                                                                                                                                                              Similarity 39; Conser
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     (TrEMBLrel.
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                         Score 243; DB 4; L
Pred. No. 2.41e-36;
22; Mismatches 38;
     Created)
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Pred. No. 2.41e-36;
22; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOLDSTEIN S.;
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                                                                                                                                                                                              cysteine-rich superfamily.";
Immunogenetics 46:276-282(1997).
EMBL; x99336; CAA67710.1; -.
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NON_TER
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Immunogenetics 46:276-282(1997).
EMBL; X99335; CAA67709.1; -.
PFAM; PF00530; SRCR; 3.
                                                                                                                                                                                                                        KANAN J.H.C., NAYEEM N., BINNS "Mechanisms for variability in ovsteine-rich superfamily.":
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                           PRINTS; PR00258; SPERACTRCPTR.
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                                                                                                                                                                                                                                                               STRAIN=SLAB/B;
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MEDLINE; 97364683.
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"Mechanisms for variability in a member
rysteine-rich superfamily ".
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                     549
                                                              490 LRLRGGDSVCSGRVEVWHSGSWGTVCDDSWSLAEAEVVCQQLGCGHALEALRDAAF-GPG 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 SGSI-WLDEVQCRGRESSLWDC.AGPWGQSDCKHEEDAGVRCS
LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
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                                           VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLG-GKGIAKQTPFSGLG 175
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>804
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Pred. No. 4.26e-36;
20; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence up
                                                                                                         Score 242;
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SCAVENGER-RECEPTOR PROTEIN; 64125250 CRC32;
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ina; Suidae;
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SIGNAL
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EMBL; AB02
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01-NOV-1999 (TrEMBLrel.
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Q9Y4V9;
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Eukaryota; Metazoa; (
Eutheria; Primates; (
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01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DMBT1/6KB.1 PROTEIN PRECURSOR.
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                            EMBL;
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AB020812;
AB020813;
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Similarity 38.2%;
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Catarrhini; Hominida
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Pred. No. 1.33e-35;
18; Mismatches 43;
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DMBT1/6KB.1 PROTEIN.

WW; 9259828E CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SLAB/B;
MEDLINE; 97364
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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EMBL; X99333; CAA67707.1; -

PROSITE; PS00420; SPERACT_RECEPT
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AB020847; BAA78577.1;
AB020848; BAA78577.1;
AB020849; BAA78577.1;
AB020850; BAA78577.1;
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AB020836 BAA78577

AB020837 BAA78577

AB020838 BAA78577

AB020839 BAA78577

AB020840 BAA78577

AB020841 BAA78577

AB020842 BAA78577

AB020843 BAA78577
SGSI-WLDEVQCRGRESSLWDCAAGPWGQSDCKHEEDAGVRCS
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                                                       VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLG-GKGIAKQTPFSGLG 175
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AB020832;
AB020833;
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the scavenger-receptor
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Qy 176 LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217

Search completed: Mon Mar 13 10:24:48 2000 Job time : 19 secs.

Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd

ch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 13 10:28:46 2000; MasPar time 6.74 Seconds 355.087 Million cell updates/sec

Tabular output not generated

Title: >US-09-147-947-6

Description: Perfect Score: Sequence: (227-327) from USO9147947A.pep (4 of 6) 757

1 IRLAGGSSVHEGRVELYHAG.....KSSWGEHNCGHKEDAGVSCT 101

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq35 1:geneseqp

Database:

Statistics: Mean 27.982; Variance 104.818; scale 0.267

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

o. Score Match Length DB ID
Match Length DB
Length DB
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Description
Pred. No.

RESULT
ID WH
AC WO
DT 1
DE H
KW H
KW 1
KW 1
KW 0

w83361 standard; Protein; w83361; 17-FEB-1999 (first entry)

875

A

Human neurotrypsin.
Human; neurotrypsin; tumour inhibition; neurological disease;
lung disease; gene therapy; drug development; stroke; brain injury;
neurodegeneration; neuroinflammatory disease; multiple sclerosis;
epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;

24 356 47.0 347 1 W64537 Human liver cell clone 25 355 46.9 489 1 W39749 Mouse marcoSR protein. 26 355 46.9 518 1 W39747 Human marcoSR protein 27 338 44.6 495 1 W39748 Human marcoSR protein 28 338 44.6 520 1 W39748 Human marcoSR protein 29 338 44.6 520 1 W39748 Human marcoSR protein 30 125 16.5 798 1 R35849 Human marcoSR protein 31 112 14.8 349 1 W35849 Human cD5 for use in T 32 88 11.6 356 1 W46917 Amino acid sequence of 33 83 11.0 1652 1 W39763 Spneumoniae ligase. 34 83 11.0 1167 1 W37700 CryET4. 35 83 11.0 1167 1 W37700 CryET4 36 83 11.0 1167 1 W37632 CryET4 protein sequenc 37 83 11.0 1167 1 R3673 CryET4 protein sequenc 38 81 10.7 323 1 R54944 Cuphea hookeriana thio 40 80 10.6 1722 1 W38429 Human dendritic cell r 41 80 10.6 1723 1 W00644 Human DEC-205. 41 80 10.6 1743 1 W00644 Human DEC-205. 42 79 10.4 1168 1 R89493 CryET class toxin 91C2 43 77 10.2 980 1 W69743 SAPAPI protein. 45 77 10.2 1130 1 R13436 Merosin M polypeptide.
47.0 347 1 W64537 46.9 489 1 W39749 44.6 9495 1 W39747 44.6 520 1 W39747 44.6 520 1 W39747 14.8 520 1 W35849 11.0 1167 1 W46917 11.0 1167 1 W476917 11.0 1167 1 W37258 11.0 1167 1 W37258 11.0 1167 1 W37258 11.0 1167 1 W37632 11.0 1167 1 W37632 11.0 1167 1 W37632 11.0 1167 1 W37632 11.0 1167 1 W39258 11.0 1167 1 W39258 11.0 1167 1 W39258 11.0 1167 1 W39258 11.0 1167 1 W39258 11.0 1167 1 W39258 11.0 1167 1 W39258 11.0 1167 1 W39258 11.0 1167 1 W39258 110.4 1168 1 R54949 110.6 1743 1 W00645 110.4 1168 1 R89493 110.2 980 1 W69741 110.2 1130 1 R14436
347 1 W64537 489 1 W39749 518 1 W39747 520 1 W39747 520 1 W39748 520 1 Y04374 798 1 Y04374 798 1 W46917 652 1 W46917 652 1 W46917 652 1 W46917 652 1 W35849 356 1 W47700 1167 1 W37258 1167 1 W37258 1167 1 W37258 1167 1 W37258 1167 1 W37258 1167 1 W37258 1167 1 W37258 1168 1 R54043 1722 1 W38429 1723 1 W00645 1743 1 W00645 1743 1 W00645 1743 1 W00645 1743 1 W00645 1743 1 W00645 1743 1 W69741 980 1 W65743 1100 1 W65743
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Human liver cell clone Mouse marcosR protein. Macrophage receptor wi Human marcosR protein Human macrophage recep Bovine enterokinase. Human colf for use in T Amino acid sequence of S. pneumoniae ligase. CryET4 protein sequenc CryET4 protein sequenc Cuphea hookeriana thio Human dendritic cell r Mouse DEC-205. Human DEC-205. Human DEC-205. SAPAPI protein. SAPAPI protein. SAPAPI protein. SAPAPI protein. SAPAPI protein.

ALIGNMENTS

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                                                                                                    Db
                                                                                                                                      Matches
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Best Local :
                                                                                                                                                                                     The present sequence is a serine procease weakfull used to is isolated from human brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs. Sequence 822 AA;
                                                                                                                                                                                                                                                                                      New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use claim 1; Page 61-65; 69pp; Japanese.
The present sequence is a serine protease designated BSSP-3, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAY-1999 (first entry)
Human serine protease BSSP-3;
Serine protease; BSSP-3; brain tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens. W09905290-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W99087 standard; Protein; W99087;
                                                                                                                                                                                                                                                                                                                                                             N-PSDB; X19024.
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24-JUL-1997; JP-213969.
(SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-1999.
                                                                   227
               287 GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                                    227 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
   287
                                                                                                                             100.0%;
Local Similarity 100.0%;
nes 101; Conservation
GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327
                                                                   IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
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                                                                                                                                  Score 757; DB 1;
Pred. No. 1.56e-71;
0; Mismatches 0
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CC and polynucleotides can be used: (i) to inhibit tumours, including concentrateses, e.g. of brain or retina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration, neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to increase survival of damaged neurons (e.g. in cases of hypoxia, ischaemia, nerve transection) and to stimulate regeneration and/or restoration of synapses; (v) to treat or prevent retinal disorders (e.g. degeneration or neoangiogenesis); (vi) to prevent apoptosis (or other causes of cell death) in the nervous system; (vii) to regenerate brain conformance, including learning and memory; (x) to treat or prevent according to treat or prevent apoptosis of the conformance of psychiatric disorders; and (xi) to treat brain or lung injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (specifically emphysema or injury associated with protease expression (spe
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Best Local S
Matches 10
                                            New human and murine neurotrypsin - used, e.g. for inhibiting tumours, treatment of neurological or lung disease, including by gene therapy and in drug development Claim 1; Page 29-32; 50pp; English.

The present sequence represents mouse neurotrypsin. Neurotrypsin pro and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or retina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse neurotrypsin.

Mouse; neurotrypsin; tumour inhibition; neurological disease;

lung disease; gene therapy; drug development; stroke; brain injury;

neurodegeneration; neuroinflammatory disease; multiple sclerosis;

epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        broughitis).
                                                                                                                                                                                                                                                           Sonderegger P;
WPI; 99-009438/01.
N-PSDB; V72590.
                                                                                                                                                                                                                                                                                                                                                            WO9849322-A1.
05-NOV-1998.
24-APR-1998; IB0625.
26-APR-1997; CH-000966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          emphysema;
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WPI; 99-0094
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05-NOV-1998.
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26-APR-1997; CH-000966.
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Similarity 100.0%;
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Pred. No. 1.56e-71;
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                          or prevent neurodegeneration
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ET OS

Bos taurus. Key

Macrophage; 16-FEB-1993 Bovine sol. R27036;

endotoxaemia; (first entry) scavanger receptor

radiolabelled; toxic;

degenerate.

Protein;

ΑA

Location/Qualifiers

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24-JUL-1998; ;
24-JUL-1997;
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                                                                                                                                                                                                                                                             New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Example 1, Page 51-54, 69pp. Japanese.

The present sequence is a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide
                                                                                                                                                                                                                                    serine protease
Sequence 761 A
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R27036 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease;
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91; Conser
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BSSP-3; brain
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91.0%;
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Pred. No. 4.
6; Mismatc
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Pred. No. 4.88e-66;
6; Mismatches 3
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4.88e-66;
3;
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21-FEB-1991; US-662227.
22-FEB-1991; US-662227.
(MASI ) WASSACHUSETTS INST TECHNOLOGY.
Krieger M;
WPI; 92-315935/38.
N-PDBB; Q28540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scavanger receptor protein inactivate endotoxin-related substances and are used in the diagnosis and treatment of endotoxaemia. They may be administered to patients at high risk of symptomatic or endotoxic shock. The fragments may also be fixed to inert supports for purifice, purposes. The fragments may be modified to have greater binding affinity for the endotoxin-related substance than the native scavanger receptor protein, or to more effectively neutralise the toxic or pathogenic effects of mols, that bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment and diagnosis of endotoxaemia and related disease states - using a polypeptide fragment of the extracellular portion of a macrophage scavenger receptor protein pisclosure; Page 38; 56pp; English.
New receptor protein - has affinity for acetylated low density lipoprotein corresponding antibodies and DNA sequences.
                                                                                                       31-MAY-1990.
14-NOV-1989; 005116.
15-NOV-1988; US-272002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the scavanger receptor protein or of organisms which express such mols. See also R27035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scavanger receptor protein. The scavanger receptor protein has a binding capacity for acetylated low density lipoprotein (LDL) and binds endotoxin. Fragments of the extracellular portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The bovine scavanger receptor protein sequence was deduced fron DNA sequence obtd. by screening a bovine lung cDNA library widegenerate probes designed based on fragments of the purified
                                               N-PSDB; Q04926
                                                                           Engellenner TJ;
                                                                                                                                                                                                                Scavenger
                                                                                                                                                                                                                                             R05509;
                                                                                                                                                                                                                                                         R05509 standard;
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                                                                                                                                                                                                             receptor protein with affinity for acylated low density
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272. .
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51. .76
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/note= "Cys-rich"
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77. .109
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Pred. No. 9.57e-36;
18; Mismatches 28
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Matches 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        progress of arteriosclerosis
Claim 2: Page 5-7; 10pp; Japanese.
The sequences given in R40802-03 represent the human scavenger
receptors I and II. These proteins may be used in the production
of antihuman scavenger receptor antibodies (AHSRA). These peptides
were used to immunise a mammal, pref. a rabbit, and anti-serum was
prepared. A monoclonal antibody was prepared from HAT-resistant
hybridoma. These antibodies may be used to determine the progress
of arteriosclerosis.
     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-1993.
16-AUG-1991; 229728.
27-AUG-1990; JP-222398.
(CHUS) CHUGAI PHARM CO LTD.
WPI; 93-277488/35.
                                                    domain
                                                                                                      Homo
                                                                                                                                 Macrophage; endotoxaemia; radiolabelled;
                                                                                                                                                          Human sol. scavanger receptor
                                                                                                                                                                                                                 R27035 standard; R27035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R40802 standard; Protein; R40802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor protein, and fragments and analogues thereof may be imobilised on a support and used in assay and purification of the aLDL target. Labelled Abs, raised to the protein may be injected into the vascular system to detect the presence of atherosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti:human scavenger receptor antibody - useful for monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q47730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J05192179-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AHSRA; mammal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plaques.
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                                                                                                                                                                                   16-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human scavenger receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity hes 54; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 55; Conse
                                                                                                        sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scavenger receptor; antihuman scavenger receptor antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        453 AA;
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der receptor I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rabbit; antiserum;
  /note= "cytoplasmic'
51. .76
                                                                          Location/Qualifiers
                                                                                                                                                                                                                                       Protein;
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Pred. No. 9.
18; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 428; DB 1; Le
Pred. No. 5.59e-35;
20; Mismatches 27;
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9.57e-36;
                                                                                                                                 toxic; degenerate.
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                                                                                                                                                                                                                                                                                                                                                327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The human scavenger receptor protein sequence was deduced from the DNA sequence obtd. by screening a platelet cDNA library with degenerate probes designed based on fragments of the purified scavanger receptor protein. The scavanger receptor protein has a binding capacity for acetylated low density lipoprotein (LDL) and binds endotoxin. Fragments of the extracellular portion of the scavanger receptor protein inactivate endotoxin-related substances and are used in the diagnosis and treatment of endotoxaemia. They may be administered to patients at high risk of symptomatic or endotoxic shock. The fragments may also be fixed to inert supports for purifice, purposes. The fragments may be modified to have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1992.
21-FEB-1992; U01370.
22-FEB-1991; US-6622:
(MASI ) MASSACHUSETTS
                                                                                                                                 WO9638725-A1.
05-DEC-1996.
30-MAY-1996; U08081.
30-MAY-1995; US-453117
                                                                                                                                                                                                         Type I macrophage scavenger receptor.
Type I macrophage scavenger receptor; SRG; kidney; cell substrate; cell attachment; atherosclerosis.
                                                                                     (SMIK ) SMITHKLINE BEECHAM CO
Brawner ME, Elshourbagy NAE,
WPI: 97-034505/03.
    Human
                               solid support
                                              mammalian scavenger
                                                             New modified human embryonic
                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                   W08077;
25-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                               W08077 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      greater binding affinity for the endotoxin-related substance than the native scavanger receptor protein, or to more effectively neutralise the toxic or pathogenic effects of mols, that bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treatment and diagnosis of endotoxaemia and related disease states - using a polypeptide fragment of the extracellular portion of a macrophage scavenger receptor protein Disclosure: Page 33: 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PDSB; Q28539
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WPI; 92-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scavanger receptor protein or of organisms which express such molsalso \ensuremath{\mathtt{R27036}}.
                                                                                                                                                                                                                                                                                                                                                                                              IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
                                                                                                                                                                                                                                                                                                                                                                 GPIWLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTCT
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    type I (W08077) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 56.5%;
Similarity 53.5%;
54; Conservative
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Page 10-13; 32pp; English.
I (W08077) and type II (W08078) macrophage scavenger
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272. .:
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110. .
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77. .10
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                                                                                                                                                                                                                                                                              Protein; 451
                                              receptor
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20; N
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Pred. No. 5.
                                              gene
                                                             kidney
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                                                                                                        Lysko
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                                                             293
                                              enhance
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5.59e-35;
ches 27;
                                                             cells
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ability to attach to
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Best Local Similarity
Matches 53; Consei
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Best Local
                                                                                                            Macrophage scavenger receptor protein.

Macrophage scavenger receptor protein, MSRP; human; lipoteichoic acid;

Macrophage scavenger receptor [MSRP; human; lipoteichoic acid;

LTA; Gram-positive bacteria; cell wall; atherosclerosis; host defence;

septicaemia; inhibitor; complement activation; cytokine release; thera

nitric oxide production; bacterial infection; septic shock.
                                                          Homo sapiens
US5624904-A.
                                                                                                                                                                                                                                                                    W19708 standard; Protein; W19708; 19-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R21512
R21512;
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Sequence 451 AA;
   29-APR-1997.
17-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The gene encoding the receptor can be expressed from a cytomegalovirus promoter in a host cell e.g. CHO cell. The resulting recombinant scavenger receptor can be used to detect modified lipoproteins or modified substances in the blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New scavenger receptor producing animal cells - which have been transformed with vector control gene for coding human scavenger receptor I or II type under control of promoter, etc. Disclosure; Fig 1; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J03290184-A.
19-DEC-1991.
06-APR-1990; 090274.
06-APR-1990; JP-090274.
(CHUS ) CHUGAI PHARMACEUTICAL KK.
WPI; 92-051436/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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52.5%;
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Pred. No. 7.19e-35;
21; Mismatches 27;
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Pred. No. 5.59e-35;
20; Mismatches 27;
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17-NOV-1993; US-154365

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This sequence represents the human macrophage scavenger receptor protein (MSRP). MSRP binds specifically to the lipoteichoic acid (LTA) residues on the Gram-positive bacterial cell wall. MSRP exhibit unusually broad binding specificity for polyanionic ligands, and have been implicated in atherosclerosis and a variety of host defence functions. This protein can be used in the method of the invention. The method of the invention is for the treatment of septicaemia caused by Gram-positive bacteria. The method comprises administration of a MSRP in an amount sufficient to
Recombinant DNA - encoding tumour associated antigen, immunoregulin-95
Disclosure; Fig 1; 69pp; English.
Immunoregulin-95 is a 90K tumour-associated antigen purified from the culture fluid of the human breast cancer cell line, CG-5, the serum of a breast cancer patient, or the ascitic fluid from an ovarian cancer patient. The native antigen, which has a mol. wt. c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of an immunoregulin (IR)-95 polypeptide Tumour associated antigen; breast cancer; cell 1: ovarian cancer; immunoregulin-95; IR-95.
                                                                                                                                                                             17-FEB-1993; E00382.
17-FEB-1992; IT-RM0100.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
(UYCH-) UNIV CHLETI ANNUNIO G D.
Azam M, Iacobelli S, Natoli C, Sures I, Ullri
                                                                                                                                                           Azam M, Iacobelli
WPI; 93-272884/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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R40172 standard;
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(UYYA ) UNIV YALE
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nes 54; Consen
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                                                                                                                                                                                                                                                                                                           /label= glycosylation site
/note= "see also AAs 125,192,362,398,551,580"
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                                                                                                                                                                                                                                                                                                                                                                                                                /label= signal
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Pred. No. 7.19e-35;
19; Mismatches 28;
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        which has a mol. wt. of
                                                                                                                                                                                 Ullrich A;
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                                                                                                                                                                               New 90K tumour-associated antigen, IR-95 - is for use in diagnosis and therapy of cancer, HIV and auto-immune diseases Claim 2; pages 45-48; 68pp; English.

90K antigen has an apparent molecular weight of approx. 95 kd. It is 290K antigen has an apparent molecular weight of approx. 95 kd. It is 4 tumour associated antigen and is elevated in the serum of patients with cancer and also in patients with HIV. It reacts with MAb Sp-2 which was prod. by immunising mice with proteins that had been released into tissue culture fluid by human MCF-7 breast cancer cells. MAb Sp-2 cell line is deposited at the Institut Pasteur, Paris, Accession number 1-1083. 90K is also present in normal subjects. It is purified from the culture fluid of the human breast cancer cell line, CG-5. N-terminal sequencing of the 90K antigen was used to design a 'quessmer' nucleotide sequence (Q48171) as a probe to screen a lambda-gtl0 library prepd. from MCF7 polyA+ RNA.

The complete nucleotide sequence of isolated clones is given in
                                                                                            Matches
                                                                                                         Query Match
Best Local
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R40213 standard; Protein;
R40213;
R40213;
O3-FEB-1994 (first entry)
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of AAs
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WPI; 93-272885/34.
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                                                                                                                                                        Sequence
                                                                                                                                                                        Q48170.
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17-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                region
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                                227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
   84
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GPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVCT
                                               MRLADGGATNQGRVEIFYRGQWGTVCDNLWDLTDASVVCRALGFENATQALGRAAFGQGS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVCT 124
                                IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is present as a high mol. wt. complex. Homology in the region 35-80 of the 90K antigen is found with type I macrophage ger receptor; sea urchin speract receptor; and human
                                                                                            Similarity 54; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 54; Conser
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IT-RM0099.
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                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= potential glycosylation site
/note= "see also AAs 125,192,363,398,551,580"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= SCRC homology region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour-associated antigen, IR-95, capable
2 (Accession No. I-1083).
antigen; breast cancer cell line CG-5;
                                                                                                         54.4%;
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53.5%;
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                                                                                          Score 412; DB 1;
Pred. No. 3.13e-33;
19; Mismatches 28
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Pred. No. 3.13e-33;
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287 GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT 327

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PS Claim 1; Page 41; 57pp; English.

CC SK-BR-3 gp97 recovered in partially proteolysed form was denatured common to the process of the proteolysed form was denatured common to the process and the proteolysed form was denatured common to the process and the principle of the professes and the resulting peptides purified and sequenced. The N-terminal sequence of gp97 was used to design common to the principle of the process and the resulting peptides purified and sequenced to design principle of the principle of the process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of process of proc
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                                    Human cytokine regulatory factor CYTRF.

Cytokine regulatory factor; cyclophilin C-associated protein;
CYTRF; CyCAP; antiinflammatory; inflammation; autoimmune disease;
multiple sclerosis; rheumatoid arthritis; ankylosing spondylitis;
meningitis; herpes encephalitis; viral meningoencephalitis;
viral hepatitis; graft rejection; graft versus host disease;
allergy; asthma; diagnosis; therapy; human.
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12-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 15
W81363 standard;
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Casipit CL, Halenbeck R, Koths KE, Taylor EW,
WPI; 93-152424/18.
New 91yco:protein complex binding to human lectin
interferes with PHA activation of lymphocytes for
preventing cancer, infectious diseases, etc.
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Gp85-97 clone
     Homo
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15-OCT-1992; U08878.
16-OCT-1991; US-777121.
15-OCT-1992; US-961404.
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     sapiens
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e 585 AA;
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19. .585
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Pred. No. 3.13e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of human cytokine regulatory factor (CYTRF), also known as cyclophilin C-associated protein (CyCAP).

Methods are provided for the modulation of cytokine production by T helper cells using CYTRF (especially human CYTRF). A pharmaceutical composition comprising CYTRF as an active agent is administered in vitro or in vivo, and can act on mature, committed Thi type T cells to decrease the production of pro-inflammatory cytokines, or to skew the commitment of precursor T helper cells to Thi or a Thi cytokine profile. The administration of CYTRF is useful in the diagnosis and treatment of autolimnume diseases (e.g. multiple sclerosis, rheumatoid arthritis, and degenerative joint diseases including ankylosing spondylitis and reactive arthritis), and inflammation caused by bacterial, viral or parasitic infection (e.g. meningitis, hereby a companion of the commitment of autolimnum companion of cytral meningencephalitis, and reactive arthritis), and hepatitis),
                                                                                                                                                                                 Matches
                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                  including response to vaccination (e.g. vaccines containing rabic varicella zoster, and measles) and skin sensitivity (e.g. graft rejection and graft vs host disease). CYTRF signalling and relationation and graft vs host disease). CYTRF signalling and relationations are also useful for modelling and screening new pharmacological agents. The administration of agents that block CYTRF action (e.g antibodies) are useful in reducing unwanted allergic responses, especially in asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reduction of pro-inflammatory cytokines in a T cell population - using cytokine regulatory factor (CYTRF), useful in the diagnosis and treatment of pro-inflammatory conditions

Disclosure; Page 47-51; 77pp; English
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17-DEC-1998.
12-JUN-1998; U12345.
13-JUN-1997; US-049578.
(STRD.) UNIV LELAND STANFORD JUNIOR
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                                                                                       227
                                           84 GPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVCT 124
                                                                                                                                 24 MRLADGGATNQGRVEIFYRGQWGTVCDNLWDLTDASVVCRALGFENATQALGRAAFGQGS 83
GPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCT
                                                                                       IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 286
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                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                  Score 412; DB 1;
Pred. No. 3.13e-33
                                                                                                                                                                                 19;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                 28;
                                                                                                                                                                                                                      Length 585
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Search completed: Mon Mar 13 10:28:55 2000 Job time : 9 secs.

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Description: Perfect Score: Title: Tabular output not generated. th_pp Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm >US-09-147-947-6 (117-217) from US09147947A.pep (3 of 6) 764 Mon Mar 13 10:25:35 2000; MasPar time 6.52 Seconds 367.019 Million cell updates/sec

(MT)

Sequence: 1 VRLRGGKNEFEGTVEVYASG.....KDIWQGGVCPQKMAAAVTCS 101

Scoring table: PAM 150 Gap 11

188963 seqs, 23686106 residues

Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35

Statistics: Mean 28.207; Variance 100.840; scale 0.280

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

114 110 9 8 7 6 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	14321	· .
234 239 239 237 237 237 237 237 225 225 225 225 225 219 219 2119	764 764 323 323	Score
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W545491 W35491 W403561 R2703562 R27036 W19708 W19708 W1597 R215152 W64590	ാനതതെ	Ħ
Mouse marcosm protein. Mouse marcosm protein. Macrophage receptor wi Human scavenger recept Human sol. scavanger r Macrophage scavenger r Type I macrophage scav Human scavenger recept Human scavenger recept Human scavenger recept Human scavenger recept Human scid sequence of Human liver cell clone Bovine sol. scavanger Scavenger receptor pro Gp85-97 clone 18 prod. Human cytokine regulat Sequence of an immunor Tumour associated 90K Sequence of a 90K tumo	seri neur	Description
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217 28.4 495 1 W39747 Human macrosR protein 217 28.4 520 1 W39748 Human macrosR protein 217 28.4 520 1 W39748 Human macrosR protein 212 28.7 1290 1 W07609 Rat von Ebner's gland 212 27.7 1290 1 W07609 Rat von Ebner's gland 212 5.0 574 1 W81362 Mouse cytokine regulat 191 25.0 574 1 W81362 Mouse cytokine regulat 113 14.8 798 1 R57283 Bovine enterokinase. 89 11.6 276 1 W00104 Pinellyl CoA synthase. 89 11.5 1130 1 R71729 Merosin major subunit 115 1130 1 R71729 Merosin major subunit 115 1130 1 R71730 Merosin major subunit 115 1130 1 R71730 Merosin major subunit 115 1130 1 R71730 Merosin major subunit 115 1130 1 R71730 Merosin major subunit 115 1130 1 R71730 Merosin major subunit 115 1130 1 R71730 Merosin major subunit 115 1130 1 R71830 Human CD5 for use in 115 1130 1 R71830 Human RLT allele D283. 80 10.5 113 1 W50883 Amino acid sequence of 115 115 115 115 115 115 115 115 115 11
495 1 way9747 Human 520 1 v04374 Human 520 1 w39748 Human 1290 1 w07609 Rat v0 574 1 w81362 Mouse 574 1 w81362 Mouse 579 1 w87328 Boving 130 1 k7728 Meros: 1130 1 k71730 Meros: 3110 1 k71730 Meros: 3110 1 k71730 Meros: 3110 1 k71730 Meros: 3110 1 k71730 Meros: 3110 1 k71730 Meros: 3110 1 k71730 Meros: 3110 1 k71730 Meros: 3110 1 k95967 Nucle: 1713 1 k95967 Human 113 1 k96463 msOS2 1706 1 k4639 msOS2 1706 1 k4631 Amino 1356 1 w46917 Amino 1297 1 k37573 Partia
1 W39747 Human 1 Y04374 Human 1 W39748 Human 1 W47609 Rat vo 1 R47784 Sequene 1 W81362 Mouse 1 W57283 Boving 1 W71729 Meros; 1 R71730 Meros; 1 R71730 Meros; 1 R71730 Nucle; 1 R95967 Nucle; 1 R95967 Human 1 W59849 Human 1 R95967 Rat R; 1 R47048 Maman, 1 W47917 Amino 1 R47048 Human 1 R47048 Human
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ALIGNMENTS

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17-FEB-1999 (first entry) Human neurotrypsin. Human neurotrypsin. Human neurotrypsin; tumour inhibition; neurological disease; lung disease; gene therapy; drug development; stroke; brain injury; neurodegeneration; neuroinflammatory disease; multiple sclerosis; epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;	LT 2 W83361 standard; Protein; 875 AA.	177 IPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217	177 IPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217		117 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGL 176	Query Match 100.0%; Score 764; DB 1; Length 822; Best Local Similarity 100.0%; Pred. No. 8.43e-76; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 822 AA;	serine protease inhibitors or expression regulators for use as drugs.	invention are used for screening for potential peptide or non-peptide	produce the enzyme or its partial segmences. Products from the present	is isolated from human brain tissue Transformants may be used to	dd69	protedse inhibitors for drug use	New serine protease expressed in brain tissue - used in screening	N-PSDB; X19024.		TRITIONS N. Vamagnohi N. Vamaghiro K.	24-JUL-1997; JP-213969.	24-JUL-1998; J03324.	04-FEB-1999.	W09905290-A1.	apiens.	protease; BSSP-3; br	ወ	13-MAY-1999 (first entry)	: Scandard, Frocern, Oss	W00087 standard. Brotpin. 822 DB

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CC laim 1; Page 20-24; Spp; English.

CC The present sequence represents human neurotrypsin. Neurotrypsin proteins

CC and polynucleotides can be used: (i) to inhibit tumours, including

CC metastases, e.g. of brain or retina; (ii) to minimise tissue damage

caused by stroke or brain injury (having a protective effect on the

penumbra zone); (iii) to treat or prevent neurodegeneration,

neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to

increase survival of damaged neurons (e.g. in cases of hypoxia,

CC ischaemia, nerve transection) and to stimulate regeneration and/or

CC causes of cell death) in the nervous system; (vii) to regenerate brain

CC degeneration or neoangiogenesis); (vi) to prevent apoptosis (or other

CC and/or nervous tissue; (viii) to treat pain; (ix) to improve brain

CC wide range of psychiatric disorders; and (xi) to treat or prevent a

CC injury associated with protease expression (specifically emphysema or

CC bronchitis).

SQ Sequence 875 AA;
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Best Local s
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24-APR-1998: IB0625.

26-APR-1997: CH-000966.

26-APR-1997: CM-000966.
                                                                                                                                                                                                                                                                                                                                      Mouse neurotrypsin:
Mouse; neurotrypsin; tumour inhibition; neurological disease;
Mouse; neurotrypsin; tumour inhibition; neurological disease;
Lung disease; gene therapy; drug development; stroke; brain injury;
neurodegeneration; neuroinflammatory disease; multiple sclerosis;
epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;
emphysema; bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
W09849322-A1.
05-NOV-1998.
             The present sequence represents mouse neurotrypsin. Neurotrypsin proteins and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or retina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the
                                                                                       New human and murine neurotrypsin - used, e.g. for inhibiting tumours, treatment of neurological or lung disease, including gene therapy and in drug development Claim 1; page 29-32; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 W83362;
17-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                     WO9849322-A1.
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26-APR-1997; CH-000966
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Similarity 100.0%;
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treat or prevent neurodegeneration,
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Pred. No. 8.43e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) t increase survival of damaged neurons (e.g. in cases of hypoxia, ischaemia, nerve transection) and to stimulate regeneration and/or restoration of synapses; (v) to treat or prevent retinal disorders (e.g. degeneration or neoangiogenesis); (vi) to prevent apoptosis (or other causes of cell death) in the nervous system; (vii) to regenerate brain and/or nervous tissue; (viii) to treat pani; (ix) to improve brain performance, including learning and memory; (x) to treat or prevent a wide range of psychiatric disorders; and (xi) to treat brain or lung injury associated with protease expression (specifically emphysema or
                                        Human SRCR protein. Scavenger receptor cysteine rich domain:
                                                                           W64591 standard;
W64591;
23-OCT-1998 (fi
              nervous system; medullo-blastoma;
autoantibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New serine protease expressed in brain tissue - used for potential serine protease inhibitors for drug use Example 1; Page 51-54; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsuruoka N, Yamaguchi N, Yamashiro WPI; 99-142942/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W99088 standard; W99088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; X19027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-1998;
24-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS SP.
WO9905290-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse serine protease BSSP-3.
Serine protease; BSSP-3; brain tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                       176 LIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTC
                                                                                                                                                                                                   225 SGPILLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSC
                                                                                                                                                                                                                                  117 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIA-KQTPFSGLG
                                                                                                                                                                                                                                                  166 IRLVGGNSGHEGRVELYHAGQWGTICDDQWDNADADVICRQLGLSGIAKAWHQAHF-GEG
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                                                                                                                                                                                                                                                                                                                                                                         protease
                                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                               42.3%;
Similarity 45.5%;
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                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                          Protein; 1785
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                                                                                                                                                                                                                                                                                             Score 323; DB 1;
Pred. No. 8.75e-25;
19; Mismatches 34
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Pred. No. 8.75e-25;
19; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                           expression
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                              glioma;
                                            SRCR; diagnosis; treatment;
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                              breast;
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                              detection;
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Best Local
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26-NOV-1997; 303394.
19-MAY-1997; US-794795.
04-FEB-1997; US-794795.
23-MAY-1996; US-017699.
(SMIK) SMITHKLINE BEECHAM CC Adamou JE, Elshourbagy NAE, G WPI; 98-001786/01.
                                                                            This sequence represents a mouse Macro scavenger receptor (MMacrosR) which is used to confirm the presence of a novel human macro scavenger receptor (HMacrosR) This polypeptide and resulting antibodies can be used to treat cardiovascular diseases, including atherosclerosis, hypertension myocardial and cerebral infarction, angina, organ failure, stroke, gangrene, and loss of function in the extremities. They can also be used to treat or diagnose various macrophage and other immune cell related host defense disorders, septic shock, pancreatitis, multiple organ failure, endotoxaemia and infections caused by gram negative and gram positive bacteria. Agonists and antagonists may also be used to treat these diseases. The polynucleotide can be used to detect mutated forms of the polynucleotide can be used to detect mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1998; E
U9-JAN-1998; E
18-JUL-1997; E
09-JAN-1997; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor, cysteine-rich) domain. The gene and encoded protein can be used to diagnose or treat tumours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist and to assess the significance of individual forms on cellular properties. The protein can be used to detect the presence of autoantibodies and antibodies which regulate its expression.
                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 45pp;
                                                                                                                                                                                                                                                                                                                                                                Human Marco scavenger receptor - used to develop products for treating e.g. cardiovascular disorders, septic chock, bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marco scavenger receptor; MarcoSR; mouse; antibodies; treatment; diagnosis; cardiovascular disease; macrophage; bacterial infecti immune cell related host cell disorder; pancreatitis; organ fail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a human protein which contains a SRCR (scavenger recenter cysteine-rich) domain. The gene and encoded protein can be used
forms of HMarcoSR which may be associated with a dysfunction and define a diagnosis of a disease (or susceptibility to a disease) resulting from altered HMarcoSR expression.

Sequence 489 AA;
                                                                                                                                                                                                                                                                                                                                              infections etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endotoxaemia;
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WPI; 98-399136/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 LIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217
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llarity 38.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agonist; antagonist; dysfunction.
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                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gross MS, Lysko PG;
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Pred. No. 1.41e-15;
18; Mismatches 43;
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Best Local
                                             and related DNA, anuscopial immune defence and phagocytosis
Claim 10; Fig 2A-B; 62pp; English.
A novel macrophage receptor with a collagenous domain, named MARCO (W03561), is a membrane-bound trimeric protein which is expressed strongly after birth in a subset of macrophages in mouse spleen and lymph nodes. It binds to bacteria but not to yeast, and probably plays a role in immune defence and/or phagocytosis. The amino acid sequence of MARCO was deduced from DNA (see also T39340) obtd. from sequence of MARCO was deduced from DNA (see also T39340) obtd. from the produced sequence of MARCO can be produced sequence of MARCO can be produced.
a mouse macrophage cDNA library.
in transformed host cells. It is
in detecting MARCO or interfering
Sequence 518 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-1996.
19-FEB-1996; FI0091.
21-FEB-1995; US-392367
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Key
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Elomaa O, Kangas M,
WPI; 96-402322/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-1997 (first entry)
Macrophage receptor with collagenous domain (MARCO)
Macrophage receptor-collagenous; MARCO; immune defe
                                                                                                                                                                                                                                                                                                                New macrophage receptor, MARCO, that by
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; T39340.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELOM/) ELOMAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KANG/) KANGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            449 GNI-WLDNVNCRGTENSLWDCSKNSWGNHNCVHNEDAGVECS 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 VRIMGGTNR--GRAEVYYNNEWGTICDDDWDNNDATVFCRMLGYS-RGRA-LSSYGG-GS 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 518
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larity 39.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
87. .89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
150. .4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gly-X-X repeats with one interruption (Ala-Glu-Lys at 174-176)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "putative N-glycosylation site" 138...140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Domain-I
/note= "hydrophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Domain-IV
/note= "collagenous structure characterised by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "putative glycosylation site"
.419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                                                                                                                                                                                                       Tryggvason K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "hydrophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "globular C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosylation
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Pred. No. 1.
21; Mismatc
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                                                                                                                                                                                                                                                                                                              that binds bacteria but not bes and antibodies, involved
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                                   with
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                             to raise antibodies its function.
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Best Local S
Matches 3
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   R27035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti:human scavenger receptor antibody - useful for monitoring progress of arteriosclerosis Claim 2: Page 5-7; 10pp; Japanese.

The sequences given in R40802-03 represent the human scavenger receptors I and II. These proteins may be used in the production of antihuman scavenger receptor antibodies (AHSRA). These peptides were used to immunise a mammal, pref. a rabbit, and anti-serum was prepared. A monoclonal antibody was prepared from HAT-resistant hybridoma. These antibodies may be used to determine the progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R40802;
                           domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; scavenger receptor; antihun AHSRA; mammal; rabbit; antiserum;
                                                                          domain
                                                                                                                         domain
                                                                                                                                                                      domain
                                                                                                                                                                                                                                                                                                                                       Macrophage; endotoxaemia; radiolabelled; toxic; degenerate
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                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-1991;
27-AUG-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arteriosclerosis.
                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S ) CHUGAI PHARM 93-277488/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGPI-WLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGG-KGIAKQTPFSGLG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNI-WLDNVNCRGTENSLWDCSKNSWGNHNCVHNEDAGVECS 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRIMGGTUR--GRAEVYYNNEWGTICDDDWDNNDATVFCRMLGYS-RGRA-LSSYGG-GS 477
                                                                                                                                                                                                                                                                                                                                                           sol. scavanger receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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larity 37.9%;
Conservative
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JP-222398
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                                                                   e= "alpha helical coiled coil"
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                           .451
                                                                                                                                                                                                                     . 76
                                                                                                                                                                                                                                         "cytoplasmic"
                                               "collagen binding"
                                                                                                                                                                                            "transmembrane
                                                                                                                                          "spacer"
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iserum; monoclonal; I
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17; M
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21; 1
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No. 2.99e-15;
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atches 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r receptor antibody;
HAT-resistant hybridoma;
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Best Local :
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17-NOV-1993; US-114365.
(MASI ) MASSACHUSETTS IN
(UYXA ) UNIV YALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9214482-A.
03-SEP-1992.
21-FEB-1992; U01370.
22-FEB-1991; US-6622:
This sequence represents the human macrophage scavenger receptor protein (MSRP). MSRP binds specifically to the lipoteichoic acid (LTA) residues on the Gram-positive bacterial cell wall. MSRP exhibit unusually broad binding specificity for polyanionic ligands, and have been implicated in atherosclerosis and a variety of host defence functions. This protein car be used in the method of the invention. The method of the invention is for the treatment of septicaemia caused by Gram-positive bacteria. The method comprises administration of a MSRP in an amount sufficient to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence obtd. by screening a platelet cDNA library with degenerate probes designed based on fragments of the purified scavanger receptor protein. The scavanger receptor protein has a binding capacity for acetylated low density lipoprotein (LDL) and binds endotoxin. Fragments of the extracellular portion of the scavanger receptor protein inactivate endotoxin-related substances and are used in the diagnosis and treatment of endotoxaemia. They may be administered to patients at high risk of symptomatic or endotoxic shock. The fragments may also be fixed to inert supports
                                                                                                                                                                                                                                                   administration of macrophage scavenger r
Disclosure; Column 23-26; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macrophage scavenger receptor protein.

Macrophage scavenger receptor protein, MSRP; human; lipoteichoic LTA; Gram-positive bacteria; cell wall; atherosclerosis; host deisepticaemia; inhibitor; complement activation; cytokine release;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for purificn. purposes. The fragments may be modified to have greater binding affinity for the endotoxin-related substance the native scavanger receptor protein, or to more effectively neutralise the toxic or pathogenic effects of mols that bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
US5624904-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment and diagnosis of endotoxaemia and related disease states - using a polypeptide fragment of the extracellular portion of a macrophage scavenger receptor protein Disclosure; Page 33: 56pp; English
                                                                                                                                                                                                                                                                                                                  Treatment of septicaemia
                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T68796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nitric oxide production; bacterial infection; septic shock.
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                                                                                                                                                                                                                                                                                                                                                                                                           Joiner KA,
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WPI; 92-31
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(MASI ) MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scavanger receptor protein or of organisms which express
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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                19-MAY-1992 (first entry Human scavenger receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 10-13; 32pp; English.
Human type I (W08077) and type II (W08078) macrophage scavenger receptors can be expressed in human embryonic kidney 293 cells following transfection of the cells with vectors carrying the respective scavenger receptor genes (T43259 and T43260). The transfected cells show an enhanced ability to attach to a solid support and are useful for screening cods. for biological activity, or for identifying antagonists of the scavenger receptor gene, e.g. sequence 451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inhibit complement activation, cytokine release or nitric oxide production induced by LTA released by the Gram-positive bacteria. In addition to treating Gram-positive septic shock, the MSRP can be used to screen for other compounds for treating Gram-positive septic shock. MSRP can also be used to purify, label or detect LTA or LTA-containing cells. MSRP, active MSRP fragments, anti-MSRP antibodies or other compounds that inhibit binding of Gram-positive bacteria to MSRP can be used to treat pathologies such as septicaemia, Gram-positive bacterial infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type I macrophage scavenger receptor.
Type I macrophage scavenger receptor; SRG; kidney; cell substrate; cell attachment; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK) SMITHKLINE BEECHAM
Brawner ME, Elshourbagy NA
WPI; 97-034505/03.
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30-MAY-1996; U08081.
30-MAY-1995; US-453117
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25-FEB-1997
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W08077 standard; Protein; 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       solid support
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mammalian scavenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New modified human embryonic kidney 293 cells - transfected with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T43259.
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                                                                                                                                                                                                                                                                                                                409
                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                        350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                                                                                                                                                                                                                                            176 LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 VRLVGGSGPHEGRVEILHSGQWGTICDDNWEVRVGQVVCRSLGYPGVQAVHKAAHF-GQG 408
                                                                                                                                                                                                                                                                                                      TGPI-WLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTCT
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                                                                                                                                                                                                                                                                                                                                                                VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGG-KGIAKQTPFSGLG
                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 31.0%;
Similarity 37.9%;
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                    Protein; 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 237; 1
Pred. No. 2.1
17; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 237; DB 1;
Pred. No. 2.99e-15;
17; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lysko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
1.99e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293
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Best Local s
Matches 3
       Best Loc
Matches
                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W64590 standa
W64590;
23-OCT-1998
                                                              This sequence represents a fragment of a human protein which contains a SRCR (scavenger receptor, cysteine-rich) domain. The gene and encoded protein can be used to diagnose or treat tumours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist and to assess the significance of individual forms on cellular properties. The protein can be used to detect the presence of autoantibodies, and Ab which regulate its expression. Sequence 666 AA;
                                                                                                                                                                                                                 Proteins containing scavenger receptor, cysteine rich domain useful for diagnosis and treatment of tumours Claim 1; Fig 1; 54pp; German.
                                                                                                                                                                                                                                                               Mollenhauer J, Pou
WPI; 98-399136/34.
N-PSDB; V49651.
                                                                                                                                                                                                                                                                                                        09-TAN-1998; D00096.
18-JUL-1997; DE-030997.
09-JAN-1997; DE-000519.
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                  WO9830687-A2.
16-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system; autoantibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human SRCR protein fragment.
Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New scavenger receptor-producing animal cells - which have been transformed with vector contg. gene for coding human scavenger receptor I or II type under control of promoter, etc. Disclosure; Fig 1; 9pp; Japanese.

The gene encoding the receptor can be expressed from a cytomegalovirus promoter in a host cell e.g. CHO cell. The resulting recombinant scavenger receptor can be used to detect modified liporoteins or modified substances in the blood.

See also R21513.
                                                                                                                                                                                                                                                                                                                                                                                                                    Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-1990; JP-090274.
(CHUS ) CHUGAI PHARMACEUTICAL KK.
WPI; 92-051436/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1991.
06-APR-1990; 090274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
J03290184-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q21549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 VRLVGGSGPHEGRVEILHSGQWGTICDDRWEVRVGQVVCRSLGYPGVQAVHKAAHF-GQG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 LIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 37.9%;
nes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGG-KGIAKQTPFSGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGPI-WLNEVFCFGRESSIEECKIRQWGTRACSHSDDAGVTCT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
       Similarity 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 AA;
    30.0%;
larity 38.2%;
Conservative
                                                                                                                                                                                                                                                                                             Poustka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             medullo-blastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666
    Score Pred. 1
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Pred.
17; M
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3 229; DB 1; Len
No. 2.22e-14;
No. 2.25e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236; DB 1;
No. 3.84e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glioma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection;
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
    2;
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    Gaps
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RESULT · 15
                                                                                                                                                                                                                                                                                                         New scavanger receptor cysteine-rich protein - the antibodies of provided the used to modulate the immune response ps (laim 7, Fig 1A-B; 46pp; Emglish.

This is the amino acid sequence of a novel protein (see W68200), considered from a cysteine-rich (SRCR) family. The sequence was deduced from an isolated cDNA clone (see V54605). Sp alpha transcripts are found in human bone marrow, spleen, lymph node, thymus and foetal liver but not in non-lymphoid tissues. Sp alpha has the same domain organisation as the extracellular region of CD5 and CD6 and is composed of 3 SRCR domains. It is capable of binding to cells of the monocyte activation, function and/or survival, and is therefore an important component in the immunoregulatory system. Wethods of using antibodies reactive with Sp alpha are disclosed. In addition, antibodies that bind to Sp alpha for modulating the interaction between Spalpha and its receptor. Sp alpha can be used in pharmaceutical compositions to regulate the immune response in, for example, autoimmune disease, viral infections, transplant
                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1998 (first entry)
Human scavenger receptor prote
SP alpha; scavenger receptor;
                                                                                                                                                                                                                                                              rejection suppression, tumour cell proliferation suppression, combined variable immunodeficiency.
Sequence 347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; V54605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-1997; US-039956.
(BRIM ) BRISTOL-MYERS S
Aruffo AA, Gebe JA, Sia
WPI: 98-495847/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1998.
05-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W68200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W68200 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection;
                                                               175 GLIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS
                                                                                                304
                                                                                                                                                                 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 LIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217
                                                                                            GVGRI-WLDNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICS
                                                                                                                           YRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLG-GKGIA-KQTPFSGL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLG-GKGIAKQTPFSGLG 175
                                                                                                                                                             LRLVGGDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGPIVLDDVRCSGNESYLWSCPHKGWLTHNCGHHEDAGVICS 161
                                                                                                                                                                                              h 29.5%;
Similarity 35.6%;
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour;
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245. ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label- Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RS SQUIBB C
Siadak AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347
                                                                                                                                                                                              Score 225; DB 1;
Pred. No. 6.04e-14;
20; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sin SP alpha.
SRCR; human; antibody; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplant rejection; therapy.
                                                                                                                                                                                                43;
                                                                                                                                                                                                                               Length 347
                                                                                              346
                                                                                                                                                                                              Indels
                                                                                                                                                                                              4;
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                4
               Y13369 stand
Y13369;
25-JUN-1999
                                                                                                                                                                                                                                                                                                               03-NOV-1
07-NOV-1
            gastrointestinal ulceration
Claim 12; Fig 54; 320pp; English.
Y13344-403 represent secreted and
                                                                                           Chen J, Goddard A, WPI; 99-229533/19.
                                                                                                             (GETH ) GENENTECH Chen J, Goddard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secreted protein; transmembrane protein; human; enterocolitis; 2011inger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999 (first Amino acid sequence
                                                             New isolated human
                                                                              N-PSDB; X52240
                                                                                                                                              24-NOV-1997;
                                                                                                                                                                                              24 - NOV - 1997;
24 - NOV - 1997;
                                                                                                                                                                                                                           21-NOV-1997,
                                                                                                                                                                                                                                                18-NOV-1997;
21-NOV-1997;
                                                                                                                                                                                                                                                                             12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                 29-0C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9914328-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-thrombotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1999
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                                                                                                                                                            US-059113

US-059115

US-059117

US-059121

US-059121

US-059121

US-059121

US-059121

US-059126

US-052287

US-062287

US-0632816

US-0632816

US-0632816

US-0632816

US-0632816

US-063281

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                                                            genes and polypeptides
                                                                                                             Gurney
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of protein PRO229
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               and
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               transmembrane
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                                                                                                            Wood WI,
                                                               used
                                                             'n.
               human
                                                             e.g.
               proteins
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of.

CC The cDNA sequences are obtained from cDNA libraries, prepared from CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. CC The encoded polypeptides have specific uses based on their homology to CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders CC associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal CC ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratincyte differentiation (e.g. psoriasis, epithelial CC cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's cuisease, ALS, neuropathies or cancer. PRO265 can be used as for survival of the reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

SQ Sequence 347 AA;

Query Match 29.5%; Score 225; DB 1; Length 347;

Best Local Similarity 35.6%; Pred. No. 6.04e-14;

Matches 37; Conservative 20; Mismatches 43; Indels 4; Gaps 4;

Search completed: Mon Mar 13 10:25:46 2000 Job time: 11 secs.

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175 GLIPIYW-SNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCS 217

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US-09-147-947-6-05.rag

(MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Mon Mar 13 10:31:53 2000;

Run on: MasPar time 6.67 Seconds 355.116 Million cell updates/sec

Tabular output not generated.

Title: >US-09-147-947-6

Description: Perfect Score: (334-433) from US09147947A.pep (5 of 6) 787

Sequence: 1 IRLAGGKGSHEGRLEVYYRG.....RRQWGRHDCSHREDVSIACY 100

Scoring table: Gap 11 PAM 150

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35

1:geneseqp

Statistics: Mean 28.512; Variance 102.112; scale 0.279

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	·	Score	Query Match	Length	DB	ID	Description	Pred. No.
	1	787	100.0	822	۳ ا	W99087	Human serine protease	3.08e-78
	2	787	100.0	875	H	W83361	neurotr	.08e-7
_	ωĭ	691	87.8	761	Н	W83362	Mouse neurotrypsin.	5.48e-67
	4	691		761	۳	88066M	Mouse serine protease	. 486
	9	412		451	Н	W19708	Macrophage scavenger r	
	ol	407	51.7	451	Н	R27035		3.88e-34
	7	407	51.7	451	سر	R40802	Human scavenger recept	3.88e-34
	80	407	:	451	Ъ	W08077	Type I macrophage scav	3.88e-34
	9	406	51.6	451	۳	R21512	Human scavenger recept	5.05e-34
_	0	404	:	453	ш	R05509	Scavenger receptor pro	
	1	404	51.3	453	۴-4	R27036	Bovine sol. scavanger	8.53e-34
	2	363		585	Н	R40172	Sequence of an immunor	
	ω	363		585	μ	R40213	Sequence of a 90K tumo	
	4	363		585	Н	R36533	clor	.82e-2
	15	363	6.	585	ب	W81363	tokine re	.82e-2
	5.	363	46.1	585	Н	R41359	Tumour associated 90K	2e-2
	17	362	46.0	666	٢	W64590	Human SRCR protein fra	4.96e-29
	8	362	46.0	1785	Ц	W64591	Human SRCR protein.	4.96e-29
	9	352	44.7	489	۲	W39749	Mouse marcoSR protein.	6.67e-28
	00	352	44.7	518	ш	W03561	Macrophage receptor wi	6.67e-28
	: :	351	44.6	1290	Ц	W07609	Rat von Ebner's gland	. 656
	j.	347	44.1	495		W39747	Human marcoSR protein	2.44e-27
	23	347	44.1	520	۳	Y04374	Human macrophage recep	.446

Human neurotrypsin.
Human; neurotrypsin; tumour inhibition; neurological disease;
lung disease; gene therapy; drug development; stroke; brain injury;
neurodegeneration; neuroinflammatory disease; multiple sclerosis;
epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;

W83361 standard; Protein; 875 W83361; 17-FEB-1999 (first entry)

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	16.	
77	77	77	77	77	77	77	77	78	78	78	81	84	96	96	105	339	339	343	343	343	347	3	١
9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.9	9.9	9.9	10.3	10.7	12.2	12.2	13.3	43.1	43.1	43.6	43.6	43.6	44.1		
1250	874	420	420	335	193	172	172	872	337	337	135	2509	798	356	349	574	574	347	347	347	520		
ᆫ	μ	Н	ب	⊷	Н	1	μ,	Н	↦	-	Н	 -	<u> </u>	ب	Н	ب	щ.	Н	۲	Н	щ		
W59361	W98698	R22219	R22215	R25063	W72157	W72210	W72084	W75912	R91314	W06579	R28982	W32881	R57283	W46917	W35849	. ● W81362	R40784	Y13369	W68200	W64537	W39748		
Drosophila melanogaste	H. pylori GHPO 686 pro	Sequence of secretory	Sequence of human inte	Soluble human IL-5 rec	HSV-2 strain SB5 Conti	HSV-2 strain SB5 Conti	HSV-2 strain SB5 Conti	Helicobacter valy1-tRN	N. gonorrhoeae glycosy	Lipo-oligosaccharide g	Thyroid N-acetyl-gluco	Protein (OA-519) cross	Bovine enterokinase.	Amino acid sequence of	Human CD5 for use in T	Mouse cytokine regulat	Sequence of cyclophili	Amino acid sequence of	Human scavenger recept	Human liver cell clone	Human marcoSR protein		
5.06e+01	5.06e+01	5.06e+01	5.06e+01	5.06e+01	5.06e÷01	5.06e+01	5.06e÷01	4.16e+01	4.16e+01	4.16e+01	2.31e+01	1.27e+01	1.08e+00	1.08e+00	1.59e-01	1.94e-26	1.94e-26	6.89e-27	6.89e-27	6.89e-27	2.44e-27		

ALIGNMENTS

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RESULT
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100.0%;
Best Local Similarity 100.0%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a serine procease work, way be used to is isolated from human brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs. Sequence 822 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W99087 standard; Protein; W99087; 13-MAY-1999 (first entry)
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24-JUL-1998; J03324.
24-JUL-1997; JP-213969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Claim 1; Page 61-65; 69pp; Japanese.

The present sequence is a serine protease designated BSSP-3, which
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WO9905290-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; X19024.
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Tsuruoka N, Yamaguchi N, Yamashiro K;
WPI; 99-142942/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                              334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEESTG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEESTG 393
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Pred. No. 3.08e-78;
0; Mismatches 0
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Claim 1; Page 20-24; 50pp; English.

Chaim 2; Chaim 3; Chaim 5; Chaim 5; Chaim 5; Chaim 5; Chaim 5; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; Chaim 6; 
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Best Local :
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Homo sapiens.
W09849322-A1.
                  gene therapy and in drug development Claim 1; Page 29-2; SOpp; English.
The present sequence represents mouse neurotrypsin. Neurotrypsin proteins and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or retha; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse neurotrypsin.

Youse; neurotrypsin; tumour inhibition; neurological disease;
lung disease; gene therapy; drug development; stroke; brain injur;
neurodegeneration; neuroinflammatory disease; multiple sclerosis;
epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;
emphysema; bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         w83362;
17-FEB-1999 (first entry)
                                                                                                                                                                                                                                             Sonderegger P;
WPI; 99-009438/01.
N-PSDB; V72590.
                                                                                                                                                                                                                                                                                                                   05-NOV-1998.

24-APR-1998; 180625.

26-APR-1997; CH-000966.

(SOND/) SONDEREGGER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sonderegger P;
WPI; 99-009438/01.
                                                                                                                                                                                       New human and murine neurotrypsin - used, e.g. tumours, treatment of neurological or lung disc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human and murine neurotrypsin - used, e.g. for tumours, treatment of neurological or lung disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-1998; IB0625
26-APR-1997; CH-0009
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9849322-Al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394
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                                                                                                                                                                                                                                                                                                                                                                                                                                            musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACY 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACY 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100;
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Similarity 100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
               to treat or prevent neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 787; DB 1;
Pred. No. 3.08e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                            disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                         for inhibiting ease, including
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Best Local
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Macrophage scavenger receptor protein.
Macrophage scavenger receptor protein; MSRP; human; lipoteichoic acid;
LITA; Gram-positive bacteria; cell wall; atherosclerosis; host defence;
septicaemia; inhibitor; complement activation; cytokine release; thera;
nitric oxide production; bacterial infection; septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-1999.
24-JUL-1998; .
24-JUL-1997; .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use Example 1; Page 51-54; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; X19027
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                                                                                                                                                                                                                                                                                                                                                                                                                                             IRLAGGKSTHEGRLEVYYKGQWGTVCDDGWTEMNTYVACRLLGFKYGKQSSVNHFDGSNR 332
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                                                                                                                                                                                                               standard;
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82; Conser
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                                                                                                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 691; DB 1; Pred. No. 5.48e-67; Mismatches 8;
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Pred. No. 5.48e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    production induced by LTA released by the Gram-positive bacteria. In addition to treating Gram-positive septic shock, the MSRP can be used to screen for other compounds for treating Gram-positive septic shock. MSRP can also be used to purify, label or detect LTA or LTA-containing cells. MSRP, active MSRP fragments, anti-MSRP antibodies or other compounds that inhibit binding of Gram-positive bacteria to MSRP can be used to treat pathologies such as septicaemia, Gram-positive bacterial infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the human macrophage scavenger receptor protein (MSRP). MSRP binds specifically to the lipoteichoic acid (LTA) residues on the Gram-positive bacterial cell wall. MSRP exhibit unusually broad binding specificity for polyanionic ligands, and have been implicated in atherosclerosis and a variety of host defence functions. This protein can be used in the method of the invention. The method of the invention is for the treatment of septicaemia caused by Gram-positive bacteria. The method comprises administration of a MSRP in an amount sufficient to inhibit complement activation, cytokine release or nitric oxide
              Krieger M;
WPI; 92-315935/38.
                                                                W09214482-A.
03-SEP-1992.
21-FEB-1992; U01370.
22-FEB-1991; US-662227.
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                                                                                                                                                                                                                                                                                                                                            Key
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                                                                                                                                                                                                                                                                                                                                                                             Macrophage; endotoxaemia;
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(UYYA ) UNIV YALE.
Joiner KA, Krieger M;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                           R27035 standard;
27035;
6-FEB-1993 (fir
                                                (MASI ) MASSACHUSETTS INST TECHNOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 VRLVGGSGPHEGRVEILHSGQWGTICDDNWEVRVGQVVCRSLGYP-GVQAVHKAAHFGQG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity nes 52; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
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                                                                                                                                 /note= "collagen binding"
341. .451
/note= "Cys-rich"
                                                                                                                                                                                       /note=
272. .3
                                                                                                                                                                                                                                                           /note=
77. .1
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mia; radiolabelled; toxic;
                                                                                                                                                                                                                                                                                                       _"cytoplasmic"
                                                                                                                                                                                                                                                                         "transmembrane"
                                                                                                                                                                                                                                     "spacer"
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Pred. No. 1.05e-34;
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350 VRLVGGSGPHEGRVEILHSGQWGTICDDRWEVRVGQVVCRSLGYP-GVQAVHKAAHFGQG 408

IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQA -- SANHFEES 391

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409 TGPIWLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTC

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Query Match
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                                                                              hybridoma. Theorem of arteriosclerosis.
                                                                                                                          Anti:human scavenger receptor antibody - useful for monitoring progress of arteriosclerosis Claim 2; Page 5-7; 10pp; Japanese.

The sequences given in R40802-03 represent the human scavenger receptors I and II. These proteins may be used in the production of antihuman scavenger receptor antibodies (AHSRA). These peptides were used to immunise a mammal, pref. a rabbit, and anti-serum was prepared. A monoclonal antibody was prepared from HAT-resistant, hybridoma. These antibodies may be used to determine the progress
                                                                                                                                                                                                                                                                                                                                                         J05192179-A.
03-AUG-1993.
16-AUG-1991;
27-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scavanger receptor protein inactivate endotoxin related substances and are used in the diagnosis and treatment of endotoxaemia. They may be administered to patients at high risk of symptomatic or endotoxic shock. The fragments may also be fixed to inert supports for purificin purposes. The fragments may be modified to have greater binding affinity for the endotoxin-related substance than the native scavanger receptor protein, or to more effectively neutralise the toxic or pathogenic effects of mols. that bind the scavanger receptor protein or of organisms which express such mols. See also R27036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; scavenger receptor; antihuman scavenger receptor antibody; AHSRA; mammal; rabbit; antiserum; monoclonal; HAT-resistant hybridoma;
                                                                                                                                                                                                                                                                                                     N-PSDB; Q47730
                                                                                                                                                                                                                                                                                                                     (CHUS ) CHUGAI PHARM CO LTD. WPI; 93-277488/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human scavenger receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scavanger receptor protein. The scavanger receptor protein has binding capacity for acetylated low density lipoprotein (LDL) arbinds endotoxin. Fragments of the extracellular portion of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence obtd. by screening a platelet cDNA library with degenerate probes designed based on fragments of the purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment and diagnosis of endotoxaemia and related disease states - using a polypeptide fragment of the extracellular portion of a macrophage scavenger receptor protein Disclosure; Page 33; 56pp; English
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Similarity 51.5%;
52; Conservation
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JP-222398.
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Pred. No. 3.88e-34;
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Pred. No. 3.88e-34;
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19-DEC-1991.
06-APR-1990; 090274.
06-APR-1990; JP-090274.
(CHUS ) CHUGAI PHARMACEUTICAL KI
WPI; 92-051436/07.
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30-MAY-1995; US-453117.
(SMIK ) SMITHKLINE BEECHAM C
Brawner ME, Elsbourbagy NAE
WPI; 97-034505/03.
N-PSDB; T43259.
                                                                                          New scavenger receptor-producing animal cells - which have been transformed with vector contg. gene for coding human scavenger receptor I or II type under control of promoter, etc. Disclosure; Fig 1; 9pp; Japanese.

The gene encoding the receptor can be expressed from a cytomegalorius promoter in a host cell e.g. CHO cell. The resulting recombinant scavenger receptor can be used to detect modified lipoproteins or modified substances in the blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure: Page 10-13; 32pp; English.
Human type I (W08077) and type II (W08078) macrophage scavenger receptors can be expressed in human embryonic kidney 293 cells following transfection of the cells with vectors carrying the respective scavenger receptor genes (T43259 and T43260). The transfected cells show an enhanced ability to attach to a solid support and are useful for screening cpds, for biological activity, or for identifying antagonists of the scavenger receptor gene, e.g. to develop agents for treatment of atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type
Type
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See also R21513.
Seguence 451 AA;
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R21512 standard;
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I macrophage scavenger receptor; SRG; kidney; substrate; cell attachment; atherosclerosis.
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R27036;
16-FEB-1993
WO9214482-A.
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Receptor protein, and fragments and analogues thereof may be imobilised on a support and used in assay and purification of the aLDL target. Labelled Abs, raised to the protein may be injected into the vascular system to detect the presence of atherosclerotic
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WPI; 90-193408/25.
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15-NOV-1988; US-27200
(MASI) Massachusetts
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23-OCT-1990
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31-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQA--SANHFEES 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 AA;
                                                                                                                                                                                                                                                                                                                                                            scavanger receptor endotoxaemia; radio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (aLDL)
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US-272002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           density lipoprotein; aLDL; atherosclerotic plaque;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                            341. .4
/note=
                                                                                                              /note=
272. .:
                                                                                                                                                             110.
                                                                                                                                                                            /note=
                                                                                       /note= "collagen binding
                                                                                                                                                                                                                                                                       /note= "cytoplasmic"
                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                    location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.3%;
                                                                                                                                                                                                                                                     .76
                                                                                                                                                                                                        . 109
                                                                                                       e= "alpha helical coiled
                                                                 .451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inst
                                                                                                                                                                                                                        "transmembrane"
                                                                                                                                                                              "spacer"
                                                                                                                                                                                                                                                                                                                                                                 radiolabelled; toxic; degenerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
19; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404; DB 1;
No. 8.53e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                      coil"
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# W09316180-A.

D 19-AUG-1993.
D 19-AUG-1993; E00382.
F 17-FEB-1993; E00382.
PR 17-FEB-1992; IT-RM0100.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA (UYCH-) UNIV CHIETI ANNUNIO G D.

A ZAMM M, IACOBELLI S, NATOLI C, Sures I, Ullrich
A ZAMM M, TARR#4/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 portion of a macrophage scavenger receptor protein

Disclosure; Page 38; 56pp; English.

The bovine scavanger receptor protein sequence was deduced from the

DNA sequence obtd. by screening a bovine lung cDNA library with

degenerate probes designed based on fragments of the purified

scavanger receptor protein. The scavanger receptor protein has a

binding capacity for acetylated low density lipoprotein (LDL) and

binds endotoxin. Fragments of the extracellular portion of the

scavanger receptor protein inactivate endotoxin-related substances

and are used in the diagnosis and treatment of endotoxaemia. They

may be administered to patients at high risk of symptomatic or

endotoxic shock. The fragments may be modified to have

for purificn. purposes. The fragments may be modified to have

the next the first protein the endotoxin-related substance than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Disclosure; Fig 1; 69pp; English.

Immunoregulin-95 is a 90K tumour-associated antigen purified from the culture fluid of the human breast cancer cell line, CG-5, the serum of a breast cancer patient, or the ascitic fluid from an ovarian cancer patient. The native antigen, which has a mol. wt. (
                                                                                                                                                                                                                                                                                                                 modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the scavanger receptor protein or See also R27035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the native scavanger receptor protein, or to more effectively neutralise the toxic or pathogenic effects of mols. that bind the scavanger receptor protein or of organisms which express such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PDSB; Q28540.

Treatment and diagnosis of endotoxaemia and related disease states - using a polypeptide fragment of the extracellular
                                                                                     Recombinant DNA - encoding tumour immuno-regulin-95
                                                                                                                                                                                                                                                                                                                                                   region
                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour associated antigen; breast brearian cancer; immunoregulin-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R40172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R40172 standard; Protein; 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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22-FEB-1991; US-662227.
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                                                                                                                                                                                                                                                                                                                                                                                                                     omo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 VRLVGGSGPHEGRVEIFHEGQWGTVCDDRW-ELRGGLVVCRSLGYK-GVQSVHKRAYFGK 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGPIWLNEVFCFPKESSIEECRIRQWGVRACSHDEDAGVTC 451
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                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                            /label= glycosylation site
/note= "see also AAs 125,192,362,398,551,580"
                                                                                                                                                                                                                                                                                                                                /label= SRCR homology region
                                                                                                                                                                                                                                                                                                                                                                   /label= signal
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19; 1
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                                                                                                       associated antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer;
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No. 8.53e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell line CG-5;
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                                                                                                                 Query Match
Best Local S
Matches 4
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Best Local
                                                                                                                                                                                                                                                                            N-PSDB; Q48170.

New 90K tumour-associated antigen, IR-95 - is for use in diagnosis and therapy of cancer, HIV and auto-immune diseases Claim 2; pages 45-48; 88pp; English.

90K antigen has an apparent molecular weight of approx. 95 kd. It is a tumour associated antigen and is elevated in the serum of patients with HIV. It reacts with MAb SP-2 which was prod. by immunising mice with proteins that had been released into tissue culture fluid by human MCF-7 breast cancer cells. MAb SP-2 cell line is deposited at the Institut Pasteur, Paris, Accession number 1-1083. 90K is also present in normal subjects. It is purified from the culture fluid of the human breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09316181-A.
19-AUG-1993.
17-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 kD, is present as a high mol. wt. complex. Homology in of AAs 35-80 of the 90% antigen is found with type I macroj scavenger receptor; sea urchin speract receptor; and human lymphocyte glycoprotein Tl/Leu-1.
                                                                                                                                                                                                                cancer cell line, CG-5. N-terminal sequencing of the 90K antigen was used to design a 'guessmer' nucleotide sequence (Q48171) as a probe to screen a lambda-gtl0 library prepd. from MCF7 polyA+ RNA. The complete nucleotide sequence of isolated clones is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of a 90K tumour-associated antigen, IR-95, capable of binding to SP-2 (Accession No. I-1083).
Tumour-associated antigen; breast cancer cell line CG-5;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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R40213;
                                                                                                                                                                                                    Q48170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYCH-) UNIV CHIETI ANNUNZIO G
(UYNY ) UNIV NEW YORK STATE.
Iacobelli S, Natoli C, Schles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 K antigen.
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                    84
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                                                                                                                                  Local Similarity
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GPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVC 123
                                                                      MRLADGGATNQGRVEIFYRGQWGTVCDNLWDLTDASVVCRALGFENATQALGRAAFGQGS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93-272885/34.
                                                 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQA-SANHFEEST 392
                                                                                                                                                                                   585 AA;
                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= potential glycosylation site
/note= "see also AAs 125,192,363,398,551,580"
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43.08;
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                                                                                                                Score 363; DB 1;
Pred. No. 3.82e-29;
25; Mismatches 31
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is found with type I macrophage
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No. 3.82e-29;
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393 GPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432

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PS Claim 1: Page 41: 57pp; English.

CC SK-BR-3 gp97 recovered in partially proteolysed form was denatured CC and reduced and the 97 and 70 kD mols. were purified using size C creation HPDC in 0.1 percent SDS. The 97 and 70 kD mols were CC digested with Lys-C protease and the resulting peptides purified and CC sequenced. The N-terminal sequence of gp97 was used to design CC degenerate primers for use in a PCR reaction on SK-BR-3 mRNA. PCR CC reactions using primer 2 in combination with primers 1 and 3 gave prods. CC of 97 and 121 bp. Further PCR using primers 2, 3 and 4 yielded DNA CC sequences of 740 and 765 respectively. A DNA sequence was obtd. from CC the PCR prods. Two additional oligonucleotide sequences were CC synthesised based on this sequence and used to probe a THP-1 cDNA CC ibrary to obtain the full-length cDNA sequence that encodes SK-BR-3 gp97. Both strands of clone 218 were sequenced. It encodes a novel CC of lymphocytes. It can be used for treating or preventing diseases that cresult from binds the Mac-2 lectin and interferes with PHA activation CC target cell. The gp. can be used in treatment of cancers, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                            multiple sclerosis; rheumatoid arthritis; ankylosing spondylitis; meningitis; herpes encephalitis; viral meningoencephalitis; viral hepatitis; graft rejection; graft versus host disease; allergy; asthma; diagnosis; therapy; human.
                                                                                                                                                                                                                                     W81363 standard; Protein; W81363; 12-APR-1999 (first entry)
                                                                                                                                                  Human cytokine regulatory factor CYTRF.

Cytokine regulatory factor; cyclophilin C-associated protein; CYTRF; CYCAP; antiinflammatory; inflammation; autoimmune dise
   Homo
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R36533;
19-AUG-1993 (first entry)
Gp85-97 clone 18 prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          target cell. The gp. can be used breast cancer. See also R36532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New glyco:protein complex binding to human lectin interferes with PHA activation of lymphocytes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-APR-1993.
15-OCT-1992; UO8878.
6-OCT-1991; US-777121.
5-OCT-1992; US-961404.
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phytoheamagglutinin; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334
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   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    GPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Halenbeck R,
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25; N
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No. 3.
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.82e-29;
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                                                                                                                                                         autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 585;
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                                                                                                                                                                                                                                                                                                    Query Match 46.1%;
Best Local Similarity 43.0%;
                                                                                                                                                                                                                                                                                                                                                                                                       allergic responses, especially in asthma. Sequence 585 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        profile. The administration of CYTRF is useful in the diagnosis and treatment of autoimmune diseases (e.g. multiple sclerosis, rheumatoid arthritis, and degenerative joint diseases including ankylosing spondylitis and reactive arthritis), and inflammation caused by bacterial, viral or parasitic infection (e.g. meningitis, herpes encephalitis, viral meningoencephalitis and viral hepatitis), and the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of the profile of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmacological agents. The administration of agents that block CYTRF action (e.g antibodies) are useful in reducing unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CYTRF), also known as cyclophilin C-associated protein (CyCAP). Methods are provided for the modulation of cytokine production by T helper cells using CYTRF (especially human CYTRF). A pharmaceutical composition comprising CYTRF as an active agent is administered in vitro or in vivo, and can act on mature, committed Thi type T cells to decrease the production of pro-inflammatory cytokines, or to skew the commitment of precursor T helper cells to Thi or a Thi cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reduction of pro-inflammatory cytokines in a T cell population - using cytokine regulatory factor (CYTRF), useful in the diagnosis and treatment of pro-inflammatory conditions
Disclosure; Page 47-51; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of human cytokine regulatory factor
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Conboy IB, Jones PP;
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12-JUN-1998;
          393
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GPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC
                                                                    GPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVC 123
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US-049578.
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Search completed: Mon Mar 13 10:32:02 2000 Job time: 9 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein · protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:32:18 2000; MasPar time 4.66 Seconds 278.133 Million cell updates/sec

Description: Perfect Score:

>US-09-147-947-6 (334-433) from US09147947A.pep (5 of 6)

1 IRLAGGKGSHEGRLEVYYRG.....RRQWGRHDCSHREDVSIACY 100

Scoring table: PAM 150 Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 27.056; Variance 104.512; scale 0.259

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Query Match	Length	BG	ID	Description	Pred. No
<u>ල</u>	412	52.4	451	μ	US-08-154-	Sequence 2, Applicatio	1.3
ν,	407	51.7	451	N	-08-97	equence 2, Applicat	4.65
ω	407	51.7	451	Н	-08-4	2, Appl	4.65
4	407	51.7	451	N	US-08-948-	2, App1	4.65
ഗ	407	51.7	451	ω	PCT-US96-0	2, Appl	4.65
σ	404	51.3	453	4	5510466-4	o. 5510466.	9.67
7	363	46.1	585	ட	US-08-473-	ce 10, z	m
œ	363	46.1	585	N	US-08-316-	, Apr	i 2.08
9	363		585	دسو	US-08-477-	10, Appl	i 2.08
10	352	44.7	489	N	US-08-794-	7, 1	2
11	352	44.7	518	ᆫ	US-08-392-	2, Appl	2.99
12	351	44.6	1290	۳	US-08-470-	2	3.81
13	347	44.1	495	N	US-08-794-	2	1.00
14	347		520	N	us-08-794-	6, Appl	1.00
15	96	12.2	356	N	US-08-681-	e 1, Appl	9.00
16	96	12.2	798	ω	PCT-US94-0	2	9
17	96	•	798	Н	US-08-200-	, Appl	9
18	84		2509	ب	US-08-469-	e 10, App	9
19	81	10.3	23	2	US-08-316-	e 11, Appl	1
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AFFLICATION NUMBER: US/08/134,363 FILING DATE: CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: PABST, PATICA L. REGISTRATION NUMBER: 31,284 REFERENCE/DOCKET NUMBER: MIT6392 TELECOMMUNICATION INFORMATION: TELEPHONE: (404)-815-6558 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 451 amino acids TYPE: amino acid STRANDEDNESS: single	EENCE ADDRESS: 1100 Peachtree Street, 1100 Peachtreet, 1100 Pea	Sequence 2, Application US/08154365 Sequence 2, Application US/08154365 Patent No. 5624904 GENERAL INFORMATION: APPLICANT: Dunne, Dana W. APPLICANT: Resnick, David APPLICANT: Kreiger, Monty APPLICANT: Kreiger, Monty APPLICANT: Joiner, Keith A. TITLE OF INVENTION: Method for Treating Gram-Positive TITLE OF INVENTION: Septicemia NUMBER OF SEQUENCES: 2	LT 1 US-08-154-365-2 STANDARD; PRT; 451 AA. xxxxxx

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Best Local Similarity 51.5%;
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                                                                                                                                                                                                                                                                                                                                Patent No. 591701.
Patent No. 591701.
Patent No. 591701.
GENERAL INFORMATION:
GENERAL INFORMATION:
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APPLICANT: Brawner, Mary E.
APPLICANT: Brawner, Mary E.
APPLICANT: NOVENTION: Attachment Enhanced 293 Cells
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           TELEFAX: (610) 270-509
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
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                                                           REGISTRATION NUMBER: P-41, 8
REFERENCE/DOCKET NUMBER: P50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Elizabeth J. Hecht
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STREET: Mailcode - UW2220, 709
CITY: King of Prussia
STATE: Pennsylvania
                                                                                                                                                   APPLICATION NUMBER: US/08/973,145 FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 19406-5090
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NCE 451 AA; 49841 MW; 1025052 CN;
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amino acid
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Pred. No. 1.37e-32
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                                                  SEQUENCE
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                                                                                                                       TELEFAX: (610) 270-50 INFORMATION FOR SEQ ID NO:
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les 52; Conser
                              TOPOLOGY: linear MOLECULE TYPE: protein 1024670 CN; UENCE 451 AA; 49762 MW; 1024670 CN;
                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                               REFERENCE/DOCKET NUMBER: SB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Brawner, Mary E.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      CITY: King of Prussia
STATE: Pennsylvania
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51.7%;
Similarity 51.5%;
52; Conservation
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Elshourbagy, Nabil A.
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51.5%;
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270: 2:
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  18;
             Score 407; DB 1;
Pred. No. 4.65e-32;
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  Mismatches
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acide
TYPE: amino
PCT-US96-08081-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: |
FILING DATE:
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                                                                                                                                                                                                            TOPOLOGY: 1; MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Jervis, Herbert H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Attachment Enhanced 293 Cells
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                                                               TGPIWLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTC 449
                                              TGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Marrow of Prussia CITY: King of Prussia STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/948,222
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Similarity 51.5%;
52; Conservative
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451 AA; 49762 MW; 1024670 CN;
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STANDARD;
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Pred. No. 4:65e-32;
18; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                         Local Similarity 51.5%;
les 52; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (610) 270-509
INFORMATION FOR SEQ ID NO:
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 16-SEP-1994
                                                             APPLICANT: KREIGER, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein JENCE 451 AA; 49762 MW; 1024670 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/08081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Jervis, Herbert H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Attachment Enhanced 293 Cells NUMBER OF SEQUENCES: 4
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CITY: King of Prussia
STATE: Pennsylvania
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                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                             MONTY; KODAMA, TATSUHIKO SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
             US/08/307,400
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Pred. No. 4.65e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08473791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-473-791-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5736340
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08473791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 STGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: N/A INFORMATION FOR SEQ ID NO:
                       NAME: Goldman, Kenneth M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 2595.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 420-3152
TELEFAX: (510) 658-5470
                                                                                             APPLICATION NUMBER: US/07/961,404 FILING DATE: 15-OCT-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTEDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,791
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Alice M.
APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koths, Kirston E.
APPLICANT: Halenbeck, Robert
APPLICANT: Taylor, Eric W.
APPLICANT: Wang, Alice M.
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APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 391,486 FILING DATE: 09-AUG-1989 APPLICATION NUMBER: 272,002
                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 453
                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                             94608
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                                                                                                                                              US/08/316,714
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Pred. No. 9.67e-32;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 MRLADGGATNQGRVEIFYRGQWGTVCDNLWDLTDASVVCRALGFENATQALGRAAFGQGS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 46.1%;
Local Similarity 43.0%;
                                                    TELEX: N/A
INFORMATION FOR SEQ ID NO:
                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/961,404
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Alice M.
APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
NUMBER OF SEQUENCES: 101
                             SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein JENCE 585 AA; 65330 MW; 1874129 CN;
                                                                                    TELEPHONE: (510) 420-3152
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                          STREET: 1400 File
CITY: Emeryville
                                                                                                             NAME: Goldman, Kenneth M. REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 25
        STRANDEDNESS:
                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                               COUNTRY: U
ZIP: 94608
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                                                                           (510) 658-5470
                                                                                                                                                                                                                                                                                                         USA
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        single
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                                                      10:
                                                                                                               2595.1
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Best Local Similarity
Matches 43; Conser
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                               TELEFAX: (510) 658-5470
TELEX: N/A
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 585 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08477674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08477674 Patent No. 5644035
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APPLICANT: Koths, Kirston E.
APPLICANT: Halenbeck, Robert F.
APPLICANT: Taylor, Eric W.
APPLICANT: Wang, Alice M.
APPLICANT: Wang, Alice M.
APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQA-SANHFEEST 392
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TOPOLOGY: li
MOLECULE TYPE:
UENCE 585 AA;
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                FILING DATE:
APPLICATION NUMBER: US/0:
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 CLASSIFICATION: 530 PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
JENCE 585 AA;
                                                                                                                      REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION: (510) 420-3152
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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CITY: I
STATE:
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
ZIP: 946
                                                                                                                                                           NAME: Goldman, Kenneth M. REGISTRATION NUMBER: 34,1
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/477,674 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                               Emeryville : CA
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                                                          585 amino acids
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                                                                                                            (510) 658-5470
                        linear
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protein
65330 MW; 1874129 CN;
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43.0%;
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65330 MW; 1874129 CN;
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Pred. No. 2.08e-27
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Best Local Similarity 43.0%;
                                            SEQUENCE
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                                                                                                                       INFORMATION FOR SEQ ID NO:
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                                                                                                                                                       REFERENCE/DOCKET NUMBER: AT TELECOMMUNICATION INFORMATION: 610-270-5219
                                                                                                                                                                                                                                                                         SOFTWARE: FastSEO for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,795
                                                                                                                                                                                                          APPLICATION NUMBER: ATG50009P FILING DATE: 22-MAY-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gross, Mitchell APPLICANT: Lysko, Paul TITLE OF INVENTION: Human TITLE OF INVENTION: eptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                           MOLECULE TYPE:
ENCE 489 AA;
                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 489 amino acid
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                 TOPOLOGY:
                                                                          STRANDEDNESS:
                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                    NAME:
                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 04-FEB-1997
                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                    STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Silt...... 709 Swedeland
                                                                                                                                            TELEFAX: 610-270-4026
            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                    H: 489 amino acids amino acid
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  Conservative
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                                                                SS: single
linear
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                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                           protein
49441 MW; 1141296 CN;
           44.78;
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Score 352;
Pred. No. 2:
23; Mismatc
                                                                                                                                                                                      34,344
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Pred. No. 2.08e-27;
25; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                     Road
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  Mismatches
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           DB 2;
2.99e-26;
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                    Length 489
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 Indels
4;
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394 VRIMGGT-NR-GRAEVYYNNEWGTICDDDWDNNDATVFCRMLGYSRGRALSS--YGGGSG 449

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Best Local
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GENERAL INFORMATION:
APPLICANT: Tryggvas
APPLICANT: Elomaa,
34 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEESTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08392367B
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            423 VRIMGGT-NR-GRAEVYYNNEWGTICDDDWDNNDATVFCRMLGYSRGRALSS--YGGGSG 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 PIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                                                                                                                              TELEX: (216) 980162
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acid
                                                                                                                                                                                    REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TRV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette, 3.50 in
MEDIUM TYPE: 720 Kb storable
COMPUTER: IBM PS/2, Model 35 s
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEESTG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee STREET: 1100 Superior Avenue STREET: Suite 700 CITY: Cleveland
                                                                                                  TOPOLOGY: L:
                                                                                                                          TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Cleveland
STATE: Ohio
                                                 h 44.7%;
Similarity 42.4%;
42; Conservative
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44114-2518
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5691197
                                                                                                                                                                                                                                                             Minnich, Richard J.
                                                                                                                                                 518 amino acids
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IBM PS/2, Mou-
TOS 5.0
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Elomaa, Outi
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                                                                                                 Linear
A; 52730 MW; 1281000 CN;
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a Collagenous Domain and the
Polypeptide Chain Encoded by
such a Sequence
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                                                Score 352; DB 1; Le
Pred. No. 2.99e-26;
23; Mismatches 30;
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Best Local Similarity 43.6%;
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                                                      US-08-794-795-2
                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                   352 GSIVLDDVACTGHEA-YLWSCSHRGWLSHNCGHHEDAGVIC 391
                                                                                                                                        334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYG-KQASANHFEEST 392
                                                                                                                                                             292 VRLVNGGDRCQGRVEILYQGSWGTVCDDSWDTKDANVVCRQLVCGWALSAPGSAHFGQGS 351
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                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
UENCE 1290 AA; 141879 MW; 9315616 CN;
                                                                                                                                                                                                                                                                                                                NAME: Wolffe, Susan A REGISTRATION NUMBER: 33,568 REFERENCE/DOCKET NUMBER: 01: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Snyder, Solomon H
TITLE OF INVENTION: Ebnerin:
TITLE OF INVENTION: Protein F
NUMBER OF SEQUENCES: 6
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                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patent In Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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1001 G Street, N.W.
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Pred. No. 3.1
26; Mismatcl
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3.81e-26;
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                                             Sequence 6, Application US/08794795
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                                                                                                                                                                                                                                                                                                          SEQUENCE
Sequence 6, Application US/08794795 Patent No. 5916766 GENERAL INFORMATION:
                                                                                                                                                                                     455 QIWLDNVQCRGTESTLWSCTKNSWGHHDCSHEEDAGVEC 493
                                                                                                                                                                                                             334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEESTG 393
                                                                                                                                                                                                                            399 VRIVGS-SNR-GRAEVYYSGTWGTICDDEWQNSDAIVFCRMLG--YSKGRALYKVGAGTG 454
                                                                                                                                                                394 PIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
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                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ATG50009P
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: AT TELECOMMUNICATION INFORMATION: 610-270-5219
                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: pepi
JENCE 495 AA; 4976
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gross, Mitchell APPLICANT: Lysko, Paul TITLE OF INVENTION: Human North TITLE OF INVENTION: eptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Han, William T REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 709 5----
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/794,795
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49764 MW; 1218428 CN;
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44.48;
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                                                                                                                   STANDARD;
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Pred. No. 1.00e-25;
21; Mismatches 30
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                 Sequence 1, Application US/08681151
                                                                  Sequence 1, Application US/08681151 Patent No. 5869637
                                                                                                                                                                                                               394 PIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                                                                                                                                                                                                                   480 QIWLDNVQCRGTESTLWSCTKNSWGHHDCSHEEDAGVEC 518
                                                                                                                                                                                                                                                        334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEESTG 393
                                                                                                                                                                                                                                                                      424 VRIVGS-SNR-GRAEVYYSGTWGTICDDEWQNSDAIVFCRMLG--YSKGRALYKVGAGTG 479
                                                                 Patent No.
                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                Match 44.1%;
Local Similarity 44.4%;
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           APPLICANT:
APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
JENCE 520 AA; 52658 MW; 1340662 CN;
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: ATG50009P
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                            APPLICANT:
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 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human TITLE OF INVENTION: eptor
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CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                    Au-Young, Janice
Bandman, Olga
Braxton, Scott Michael
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Lysko, Paul
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Adamou, John
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A NOVEL HUMAN KALLIKREIN
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Pred. No. 1.00e-25;
21; Mismatches 30
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COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: PASTSEQ Version 1.5
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,151
FILING DATE: HEFEWITH
CLASSIFICATION UMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 9F-0074US
REGISTRATION NUMBER: 9F-0074US
REGISTRATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFOONMICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEYAX: 4
                                                                                                                  Query Match 12.2%; Score 96; DB 2; Length 356; Best Local Similarity 34.1%; Pred. No. 9.00e-01; Matches 14; Conservative 11; Mismatches 13; Indels
27 VCADGWQEILSQLACKQMGL--GEPSVTKLIQEQEKEPRWL 65
|| || || : : |:|:|: | : : : : | | | |
358 VCDDGWTELNTYVVCRQLGFKYGKQASANHFEE-STGPIWL 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                     ω
                                                                                                                     Gaps
                                                                                                                     2
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Š completed: Mon Mar 13 10:32:25 2000
ne : 7 secs.

334-43} SCRC3 US-09-147-947-6-05.rpr Uschts 2003

**************** (MT)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:31:24 2000; MasPar time 10.32 Seconds 457.141 Million cell updates/sec

Description: Perfect Score: Title: >US-09-147-947-6 (334-433) from US09147947A.pep (5 of 6)

Sequence: 1 IRLAGGKGSHEGRLEVYYRG.....RRQWGRHDCSHREDVSIACY 100

Scoring table: PAM 150 Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: pir62 1:pir1 2:pir2 3:pir3 4:pir4 Mean 37.820; Variance 61.366; scale 0.616

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Score	Query	Length	DB	ID	Description	Pred. No.
ш	691		761	2	JC5759	brain-specific serine	2.59e-143
2	419	53.2	918	N	JC4361	eceptor	.42e-75
ω	413		453	N	S08276	tor I, mag	.09e-7
4	412	•	1116	N	S36077	0 antigen - k	e-7
Ŋ	412		1149	N	138006	0 antigen (e	.24e-7
σ	412		1151	N	I38004	antigen (.24e-7
7	412	•	1156	N	I38005	_	
æ	412	•	2153	N	T14893	6	1.24e-73
9	407	51.7	451	N	A38415	Œ	
10	405	•	454	N	146862		6e-7
11	397		454	N	A44407	macrophage scavenger	.65e-7
12	393		458	N	B44407		.31e-
13	391		1436	N	A46496	\vdash	.63e-6
14	374		600	N	S56744	clone p	.15e-6
15	363		585	N	A47161	Mac-2-binding glycopr	.75e-
16	352	44.7	518	N	A55840		ပ်
17	351	٠	1290	N	A57190	ebnerin precursor - r	.53e-
18	350	•	577	N	A53202	cyclophilin C-associa	.31e-5
19	346	•	504	N	674	mucin (clone pGM31-1)	.19e-5
20	293	•	468	N	7	glycop	.58e-
21	281	•	532	N	A32751	speract receptor prec	.95e-
22	281	٠	626	N	149100	recursor .	.95e-
23	114	14.5	495	Ь	S11270		.39e-

4 4 5	. 4.	42	41	40	39	38	37	36	35	34	သ	32	31	30	29	28	27	26	25	24
82	82	83	83	84	84	86	88	88	88	89	90	91	91	92	93	96	99	99	105	106
10.4		10.5	10.5		10.7	10.9	11.2	11.2	11.2	11.3	11.4	11.6	11.6	11.7	11.8	12.2	12.6	12.6	13.3	13.5
340	149	670	411	2509	2504	583	1113	494	333	2206	501	2616	613	202	558	1035	1019	442	495	1034
NK	N	N	N	N	۲	N	N	۲	N	N	۳	2	2	N	N	ட	Н	N	ы	ᆫ
C71266	A58801	G71251	C69534	G01880	A57788	A29154	JE0315	A29079	T15257	JC5280	S43536	A57096	S15468	T01605	T15448	A43090	A56318	I47074	A26396	A53663
hypothetical protein conserved hypothetica	mannose-specific lect	probable DNA helicase	probable acyl-CoA deh	fatty-acid synthase (fatty-acid synthase (complement factor I (low-density lipoprote	lymphocyte surface gl	hypothetical protein	voltage-dependent cal	T-cell surface glycop	nudel protein precurs	complement C3b/C4b in	blue copper-binding p	hypothetical protein	enteropeptidase (EC 3	enteropeptidase (EC 3	gene CD5 protein - sh	T-cell surface glycop	enteropeptidase (EC 3
9.61e-01 9.61e-01	9.61e-01	6.75e-01	6.75e-01	4.72e-01	4.72e-01	2.29e-01	1.10e-01	1.10e-01	1.10e-01	7.57e-02	5.21e-02	3.58e-02	3.58e-02	2.45e-02	1.67e-02		1.61e-03	1.61e-03	1.44e-04	9.57e-05

ALIGNMENTS

333 PIWLDDVSCSGKEVSF1QCSRRQWGRHDCSHREDVGLTCY 372	Db 3:
334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEESTG 393	Qy 33
273 IRLAGGKSTHEGRLEVYYKGQWGTVCDDGWTEMNTYVACRLLGFKYGKQSSVNHFDGSNR 332	Db 27
Similarity 82.0%; 82; Conservative	Best ^I Matche
Query Match 87.8%; Score 691; DB 2; Length 761;	Query
#leng	SUMMARY
<pre>predicted\ 562,612,711</pre>	562,6
569	93,52
	517-755
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386-486 #domain scavenger receptor cysteine-rich #status	386-4
	166-2
#domain	163-
	85-157
	FEATURE
gl	KEYWORDS
'ICATION #superfamily-trypsin homology; scavenger receptor	CLASSIFICATION
##experimental_source_brain	#
ferenc	#
##residues 1-761 ##label YAM	#
E P	į
ccession JC5759	# acc
Cystelle IlCLIES.	#cros
	#title
journal Biochem. Biophys. Res. Commun. (1997) 239:386-392	#jou
Tsufimura, r.; ramagnichi. N	#auciois
JC5759	REFERENCE
JC	ACCESSIONS
24-Jan-1998 #sequence_revision l3-Mar-1998 #text_change 17-Mar-1999	DATE
	ORGANISM
JC3/39 #Type complete brain-specific serine proteinase (EC 3.4.21) - mouse	TITLE
	RESULT

δÃ

DATE

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KEYWORDS
FEATURE
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ENTRY
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                                                                                                  ACCESSIONS
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Best Local 9
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896-918
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356-389
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#title
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234-267
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40,545,575,585,
814
                        #journal
                                                              #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ches
                                                                                                                                                                                                                                                                                                393 GPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                                                                                                                                                                                                                                                                                                                     525 GQIWLDDVNCYGQESSLARCNHSGWGRHNCGHNEDASVIC 564
                                                                                                                                                                                                                                                                                                                                                                       334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASAN-HFEEST 392
                                                                                                                                                                                                                                                                                                                                                                                               466 VRLVGG-GWCQGRVEVYYAGSWGTVCDDSWDRQDAEVVCRQLSCGYAVSAPSNAHFGVGS 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-918 ##label MAY
##cross-references GB:U20652; NID:g790233; PID:g790234
This protein is rich in cysteine and plays a role in contacts and cell activation or differentiation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 PIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACY 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
52; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system
                                                                                                                                                                     $08276 #type complete
LDL receptor I, macrophage - bovine
macrophage scavenger receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mayer, W.E.; Tichy, H.

Gene (1995) 164:267-271

A CDNA Clone from the see-lamprey Petromyzon marinus coding
for a scavenger receptor Cys-rich (SRCR) domain protein.
Kodama, T.; Freeman, M.; Rohrer,
Matsudaira, P.; Krieger, M.
Nature (1990) 343:531-535
Type I macrophage scavenger recep
                                                                                                                                     macrophage scavenger receptor type I
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycoprotein; growth factor; receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #superfamily EGF homology; scavenger receptor cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JC436
                                                                                S08276
                                                                                                       S0827
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larity 52.0%;
Conservative
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                                                                                                                   20-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #binding_site carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain EGF homology #label
#domain EGF homology #label
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#domain scavenger receptor cysteine-rich domain homology
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#label SRC2\
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h 918 #mol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #molecular-weight 101417 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane #status predicted intracellular #status predicted
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EGF homology #label
EGF homology #label
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 419; DB 2; Le
Pred. No. 2.42e-75;
21; Mismatches 25;
scavenger receptor contains alpha-helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EG1/
EG2/
EG3/
EG4/
                                                          ۲.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 918;
                                                          Zabrecky,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (covalent) #status
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#label INT\
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Best Local
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248,266
                      816-920
                                                          711-814
                                                                                                  575-678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 GTGPIWLNEVFCFGKESSIEECRIRQWGVRACSHDEDAGVTC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 VRLVGGSGPHEGRVEIFHEGQWGTVCDDRW-ELRGGLVVCRSLGYK-GVQSVHKRAYFGK 409
                                                                                                                                                                                                                                                                                                                                                                                                               ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTEL-NTYVVCRQLGFKYGKQASANH--FEE 390
                                                                                                                                                                                                                                                                                                                                                       ##cross-references EMBL:Z22968; NID:g312141; PID:g312142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##note
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Similarity 52.9%;
54; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Law, S.K.; Micklem, K.J.; Shaw, J.M.; Zhang, X. Willis, A.C. Mason, D.Y.

Eur. J. Immunol. (1993) 23:2320-2325

A new macrophage differentiation antigen which the scavenger receptor superfamily.

nces MUID:93380506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $36077  #type complete
M130 antigen - human
#formal_name Homo sapiens #common_name man
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #superfamily unassigned collagens; scavenger receptor
    cysteine-rich domain homology
    alternative splicing; coiled coil; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                  I38003
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                                                                                                                                                                                                                                                                                                                                     #superfamily scavenger receptor
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                                                          #domain
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Pred. No. 7.09e-74;
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GB:X54182; NID:g734;
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                      domain
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Best Local Similarity 48.5%;
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#journal Eur. J. Immunol. (1993) 23:2320-2325

#title A new macrophage differentiation antigen which
the scavenger receptor superfamily.

#cross-references MUID:93380506
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FICATION #superfamily scavenger receptor cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            773 TGPIWLDEMKCNGKESRIWQCHSHGWGQQNCRHKEDAGVIC 813
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                                                                                                                                                                                                                               y Match 52.4%;
Local Similarity 48.5%;
                                                                                                                                                            LRLVNGGGRCAGRVEIYHEGSWGTICDDSW-DLSDAHVVCRQLGCGEAINATGSAHFGEG 805
                                                                                    TGPIWLDEMKCNGKESRIWQCHSHGWGQQNCRHKEDAGVIC 846
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                                                                                                                                         IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTEL-NTYVVCRQLGFKYGKQASAN-HFEES 391
                                                                 TGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                                                                                                                                                                                                  49;
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M130 antigen (extracellular variant) - human
#formal_name Homo sapiens #common_name man
17-May-1996 #sequence_revision 17-May-1996 #text_change
02-Aug-1996
I38004
                                                                                                                                                                                                                                                                                    #length 1149 #molecular-weight 124328 #checksum
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#label SRC9
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#label SRC7\
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Pred. No. 1.24e-73;
25; Mismatches 24
                                                                                                                                                                                                              Score 412; DB 2;
Pred. No. 1.24e-73;
25; Mismatches 24
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Best Local Similarity 48.5%;
Matches 49; Conservative
                                                                                                       #journal Eur. J. Immunol. (1993) 23:2320-2325
#title A new macrophage differentiation antigen which
the scavenger receptor superfamily.
#cross-references_MUID:93380506
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#title A new macrophage differentiation antigen which is a member of
the scavenger receptor superfamily.
#cross-references MUID:93380506
                                                                                                                                                                                                        #authors
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                                    ##molecule_type mRNA
##residues 1-1156 ##label RES
                                                                           ##Status
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##cross-references EMBL:222970; NID:g312145; PID:g312146
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                                                                                              I38005
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M130 antigen (cytosolic variant 2) - human
#formal_name Homo sapiens #common_name man
17-May-1996 #sequence_revision 17-May-1996
07-Feb-1997
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                                                                         preliminary; translated
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#label SRC7\
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Pred. No. 1.24e-73;
25; Mismatches 24
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Local Similarity 48.5%;
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Immunogenetics (1999) 49:773-786
Origins of immunity: transcription factors and homologs of
effector genes of the vertebrate immune system expressed
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T14893
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#formal_name Strongylocentrotus purpuratus
purple urchin
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Pred. No. 1.24e-73;
25; Mismatches 24
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Pred. No. 1.24e-73;
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#title Human macrophage scavenger receptors: primary structure, expression, and localization in atherosclerotic lesions.
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##molecule_type nucleic acid
##residues 155-272 ##label EMI_
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##residner
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Similarity 51.5%;
52; Conservation
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Structure, organization, and chromosomal mapping of 1
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#superfamily unassigned collagens;
Bickel, P.E.; Freeman, M.W.
J. Clin. Invest. (1992) 90:1450-1457
Rabbit aortic smooth muscle cells express inducible
macrophage scavenger receptor messenger RNA that is
                                                                                                                                                                                   macrophage scavenger receptor type I - rabbit
#formal_name Oryctolagus cuniculus #common_name domestic
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Pred. No. 2.07e-72;
18; Mismatches 28
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#accession A44407
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##note sequence extracted from NCBI backbone (NCBIP:123206)
IFICATION #superfamily unassigned collagens; scavenger receptor
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##molecule_type nucleic acid

1-454 ##label DOI
                                                                                           392
                                                                                                                                                                              334 IRLAGGKGSHEGRLEVYYRGOWGTVCDDGWTELNT-YVVCRQLGFKYGKQASAN-HFEES
                                                                                                                                                                                                                      353 VRLVGGRGPHEGRVEILHNGQWGLVCDDHW-ELRAGQVVCRSLGYRGVKSVHKKAYFGQG 411
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##cross-references GB:L11693; NID:g165508; PIDN:AAA31402.1; PID:g165509
FICATION #superfamily unassigned collagens; scavenger receptor
cysteine-rich domain homology
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Local Similarity 50.5%;
Local Similarity 50.5%;
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                                                                                                                                                                                                                                                                     h 50.4%;
Similarity 49.5%;
50; Conservative
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Charged collagen structure mediates the recognition of
  B44407
                                                                                                                                                                                                                                                                                                                                                               #length 454
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16-Jul-1999
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#label SRC
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#type complete
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                                                                                                                                                                                                                                                                     Score 397; DB 2; Length 454; Pred. No. 5.65e-70; 22; Mismatches 26; Indels
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Pred. No. 6.36e-72;
22; Mismatches 25
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structures and high and low affinity ligand binding properties of murine type I and type II macrophage scavenger receptors.

#accession 156334
##status
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#title An ancient, highly conserved family of cysteine-rich produced by cloning type I and type II murine macrophage scavenger receptors.

#cross-references MUID:91062370
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#accession B44407
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                                                                                                                                                                      393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##residues 5-458 ##label RES
##cross-references GB:L04974; NID:g293745; PIDN:AAA39747.1; PID:g293746
##CICATION #superfamily unassigned collagens; scavenger receptor
cysteine-rich domain homology
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##molecule_type nucleic acid
##residues 1-458 ##label DOI
##experimental_source macrophage-like cell line p388D
##note sequence extracted from NCBI backbone (NCBIP:123207)
                                                                                                                                                                                                            417 GPIWLNEVMCFGRESSIENCKINOWGVLSCSHSEDAGVTC 456
                                                                                                                                                                                                                                                          334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQA-SANHFEEST 392
                                                                                                                                                                                                                                                                               ##residues 349-458 ##label FRE 349-458 ##label #RE 349-458 ##label ##residues 349-458 ##label #RE
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Local Similarity 47.0%;
hes 47; Conservative
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                                                                                                                                                                  GPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC
A46496 #type complete antigen WC1.1 precursor - bovine formal_name Bos primigenius taurus #common_name cattle 18-Jun-1993 #sequence_revision 19-May-1994 #text_change
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#formal_name Mus musculus #common_name house mouse
30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change
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Ashkenas, J.; Penman, M.; Vasile,
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Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger
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A44407
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Pred. No. 5.31e-69;
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25-131
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#title Molecular characterization of the WC1 antigen expressed

specifically on bovine CD4-CD8- gamma delta T lymphocytes

#cross-references_MUID:93056489
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                                                                                                              931 LRLVDGGGPCGGRVEILDQGSWGTICDDDW-DLDDARVVCRQLGCGEALNATGSAHFGAG 989
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                                          990 SGPIWLDDLNCTGKESHVWRCPSRGWGRHDCRHKEDAGVIC 1030
                                                                                 334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELN-TYVVCRQLGFKYG-KQASANHFEES 391
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##cross-references EMBL:X63723; NID:gl3; PID:gl4
##experimental_source CD4-CD8- gamma delta T lym
  392
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                                                                                                                                                                      y Match 49.7%;
Local Similarity 47.5%;
hes 48; Conservative
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TGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
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Members of the novel WCl gene family are differentially expressed on subsets of bovine CD4-CD8- gamma delta T
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A46496; I45834; S19913
A46496
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#label SR11
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#label sr05\
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Pred. No. 1.63e-68;
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#accession A47161
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##molecule_type mRNA
##residues 1-585 ##label
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##cross-references GB:L13210;
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##residues 1-600 ##label NUN
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Similarity 50.5%;
51; Conservati
                                                                                         Ullrich, A.; Sures, I.; D'Egidio, M.; Jallal, B.; Powell, T.J.; Herbst, R.; Dreps, A.; Azam, M.; Rubinstein, M.; Natoli, C.; Shawyer, L.K.; Schlessinger, J.; Iacobelli, J. Biol. Chem. (1994) 259:18401-18407
The secreted tumor-associated antigen 90K is a potent immustimulator.
                                                                                                                                                                                                                                                                                                                                                                                  Koths, K.; Taylor, E.; Halenbeck, R.; Casipit, C.; Wal
J. Biol. Chem. (1993) 268:14245-14249
Cloning and characterization of a human Mac-2-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A47161 #type complete
Mac-2-binding glycoprotein precursor - human
90K tumor-associated protein precursor
#formal_name Homo sapiens #common_name man
05-May-1995 #sequence_revision 05-May-1995 #text_change
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mucin (clone pGM7-1) - bovine (fragment)
#formal_name Bos primigenius taurus #common_name cattle
27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                protein, a new member of the superfamily defined by macrophage scavenger receptor cysteine-rich domain.
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NID:g307152; PID:g307153
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#accession A41005
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ches 4
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journal Biochem. Biophys. Res. Commun. (1994) 201:1366-1375
title Identification of human melanoma cellular and secreted
pross-references MUID:94296411
recession PC2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##molecule_type protein

19-22,'G',24-27,'XX',30 ##label ROS

the reported molecular weight of this protein,

designated Mac-2-binding glycoprotein 2 (MZBP-2), was

70K; the amino-terminal sequence of a related form of

98K, designated MZBP-1, could not be determined

IFICATION #superfamily scavenger receptor cysteine-rich domain homology

extracellular protein; glycoprotein
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##residues 19-26 ##label IN2
##note the reported molecular weight of this protein was 70K
                                                                                            393 GPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                                                                                                                                                                             334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQA-SANHFEEST 392
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##residues 19-38 ##label INO
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##residues 19-24,'C',26-40 ##label IAC
                                                                                                                                                                                                                                                                                              y Match 46.1%;
Local Similarity 43.0%;
hes 43; Conservative
                                                                                                                                            84 GPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVC 123
                                                                                                                                                                                                                      Rosenberg, I.; Cherayil, B.J.; Isselbacher, K.J.; Pillai, S. J. Biol. Chem. (1991) 266:18731-18736
Mac-2-binding glycoproteins. Putative ligands for a cytosolic beta-galactoside lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the reported molecular weight of this protein was PC2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tacobelli, S.; Bucci, I.; d'Egidio, M.; Giuliani, C.; Natoli, C.; Tinari, N.; Rubistein, M.; Schlessinger, J. FEBS Lett. (1993) 319:59-65 Purification and characterization of a 90 kDa protein released from human tumors and tumor cell lines.
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                                                                                                                                                                                                                                                                                                                                                                                               #length 585  #molecular-weight 65330  #checksum 2263
                                                                                                                                                                                                                                                                                                                                                                                                                                           #domain signal sequence #status predicted #label SIG\
#domain scavenger receptor cysteine-rich domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                         #label SRC
                                                                                                                                                                                                                                                                                            Score 363; DB 2; Length 585; Pred. No. 9.75e-62; 25; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                              Gaps
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h_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:30:22 2000; MasPar time 6.44 Seconds 463.783 Million cell updates/sec

Description: Perfect Score: Sequence: >US-09-147-947-6 (334-433) from US09147947A.pep (5 of 6) 787 1 IRLAGGKGSHEGRLEVYYRG.....RRQWGRHDCSHREDVSIACY 100

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot38 1:swissprot

Statistics: Mean 38.688; Variance 57.261; scale 0.676

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

· त	Score	Query Match	Length	DB	ID	Description	Pred. No.
-ب	787	100.0	875	ר	NETR_HUMAN	NEUROTRYPSIN PRECURSOR	1.39e-183
N	691	87.8	761	Н			5e-15
ω	413	52.5	453	μ,	MSRE_BOVIN	MACROPHAGE SCAVENGER R	7.34e-81
4	407	51.7	451	щ	MSRE_HUMAN	MACROPHAGE SCAVENGER R	2.93e-79
U	405	51.5	454	Н	MSRE_RABIT	MACROPHAGE SCAVENGER R	
σ	393	49.9	458	Н	MSRE_MOUSE	MACROPHAGE SCAVENGER R	1.56e-75
7	391	49.7	1436	ب	WC11_BOVIN	ANTIGEN WC1.1.	.32e-
œ	293	37.2	468	Н	CD6_HUMAN	T-CELL DIFFERENTIATION	.22e-4
ဖ	281	35.7	532	\vdash	SPER_STRPU	EGG PEPTIDE SPERACT RE	2.60e-46
10	114	14.5	495	Н	CD5_BOVIN	T-CELL SURFACE GLYCOPR	4.72e-07
11	106	13.5	1034	Н	ENTK_PIG	ENTEROPEPTIDASE PRECUR	1.75e-05
12	105	13.3	495	Н	CD5_HUMAN	T-CELL SURFACE GLYCOPR	2.72e-05
13	100	12.7	492	_	TMS2_HUMAN	TRANSMEMBRANE PROTEASE	
14	100	12.7		↦	ENTK_MOUSE	ENTEROPEPTIDASE (EC 3.	
15	99	12.6	1019	ب	ENTK_HUMAN	ENTEROPEPTIDASE PRECUR	3.68e-04
16	96	12.2		μ.	ENTK_BOVIN	ENTEROPEPTIDASE PRECUR	
17	91	11.6	2616	ш	NDL_DROME	SERINE PROTEASE NUDEL	.046
18	90	11.4	491	μ	CD5_RAT	T-CELL SURFACE GLYCOPR	1.55e-02
19	88	11.2	494	سر	CD5_MOUSE	T-CELL SURFACE GLYCOPR	3.46e-02
20	86	10.9	583	μ	CFAI_HUMAN	COMPLEMENT FACTOR I PR	7.62e-02
21	84	10.7	2504	<u>_</u>	FAS_HUMAN	FATTY ACID SYNTHASE (E	1.66e-01
22	82	10.4	306	ш	YE16_YEAST	ם	.55e
23.	80	10.2	756	ب	RIR1_HAEIN	RIBONUCLEOSIDE-DIPHOSP	7.51e-01

4 4 4 5	43	42	41	40	39	38	37	3 6	35	34	33	32	31	30	29	28	27	26	25	24
73 73	74	74	74	74	74	75	75	75	76	76	76	77	77	77	77	77	77	77	77	79
φ. ω.ω	9.4	9.4	9.4	9.4	9.4	9.5	9.5	9.5	9.7	9.7	9.7	9.8	9.8	9.8	9.8	9.8	9.8	9.8	9.8	10.0
210 332	1343	639	573	200	108	1884	584	330	530	287	287	1054	997	874	841	639	420	172	146	1885
μμ	ш	ш	ш	Н	Ь	Н	Н	ப	μ	Н	Н	Н	Н	Н	μ	Н	1	Н	j	Н
YAC9_MAIZE GLYG_RAT	RPOB_HAEIN	HTPG_TREPA	CATT_YEAST	ARFM_CAEEL	RPOM_METJA	RRPO_ACLSP	CO8A_HUMAN	ASNA_HAEIN	YA9A_SCHPO	NIFH_FRAAL	NIFH_FRASP	RDGB_DROME	YNM3_YEAST	SYV_HELPY	YAGX_ECOLI	YAJ9_SCHPO	IL5R_HUMAN	UL45_HSV23	HBRH_CHICK	RRPO_ACLSA
TRANSPOSABLE ELEMENT A GLYCOGENIN-1 (EC 2.4.1	DNA-DIRECTED RNA POLYM	HEAT SHOCK PROTEIN HTP	CATALASE T (EC 1.11.1.	GTP-BINDING ADP-RIBOSY	DNA-DIRECTED RNA POLYM	RNA-DIRECTED RNA POLYM	COMPLEMENT COMPONENT C	ASPARTATE AMMONIA LIG	HYPOTHETICAL 54.2 KD S	NITROGENASE IRON PROTE	NITROGENASE IRON PROTE	RETINAL DEGENERATION B	HYPOTHETICAL 110.9 KD	VALYL-TRNA SYNTHETASE	HYPOTHETICAL 91.2 KD P	HYPOTHETICAL 74.4 KD P	INTERLEUKIN-5 RECEPTOR	PROTEIN UL45 HOMOLOG (HEMOGLOBIN RHO CHAIN.	RNA-DIRECTED RNA POLYM
9.19e+00 9.19e+00	6.51e÷00	6.51e+00	6.51e+00	6.51e+00	6.51e+00	4.59e+00	4.59e+00	4.59e+00	3.22e+00	3.22e+00	3.22e+00	2.25e+00	2.25e+00	2.25e+00	2.25e+00	2.25e+00	2.25e+00	2.25e+00	2.25e+00	1.09e÷00

ALIGNMENTS

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          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                             Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                          GSCHWEND T.P., KRUEGER "Neurotrypsin, a novel nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1999 (Rel. 39, C
15-DEC-1999 (Rel. 39, I
15-DEC-1999 (Rel. 39, I
NEUROTRYPSIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                         Molecular cloning of a novel brain-specific serine ringle-like structure and three scavenger receptor hotifs.";
                                                                                                                                                                                                                                                           YAMAGUCHI N.;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEASE 3) (BSSP-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NETR_MOUSE 008762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEESTG 446
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                                                                                                                                                                Chem. Blophys. Res. Commun. 239:386-392(1997).
FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH LEARNING AND MEMORY OPERATIONS.
TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL CORTEX, HIPPOCAMPUS
                                                                                                SIMILARITY: CONTAINS 1 KRINGLE DOMAIN. SIMILARITY: CONTAINS 3 SRCR DOMAINS.
                                                                                                                            musculus
                                                                                                                         TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACY 486
                                                                                                                                                                                                                                                                                                                  Cell. Neurosci.
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; 98008848.
A Y., YAMASHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08;
similarity 100.08;
100: Common 100.08;
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875 1
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97011
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                                                                                                                                                                                                                                                                                                              9:207-219(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
PR (EC 3.4.21.-) (MOTOPSIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                     S.R., KOZLOV S.V., multidomain serine
                                                                                                                                                                                                                                                                     K., TSURUOKA N., NAKAZATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , WM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score Pred. 0; N
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POTENTIAL.
; 67D5272B CRC32;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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ZYMOGEN ACTIVATION REGION
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No. 1.39e-183;
                                                                                                                                  FAMILY
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                                                                                                                                                                                                                                                                                                                                       protease expressed
                                                                                                                                                                                                                                                                                                                                                   WOLFER D.P.,
                                        as its content is in
                  http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                    receptor
                                                                                                                                  S1;
                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                               Уď
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Mus.
                                                                                                                                                                                                                                   protease with cysteine-rich
                                                                                                                                  KNOWN
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                                and
                                                                EMBL outstation
                                                                 a collaboration -
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Best Local S
Matches 8
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EMBL; D89871; BAA23986.1; -
MGD; MGI:1100881; PRSS12.
PFAM; PF000530; SRCR; 3.
PFAM; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                      MSRE_BOVIN STANDARD; PRT; 453 AA. P21758; O1-MAY-1991 (Rel. 18, Created) O1-MAY-1991 (Rel. 18, Last sequence update) O1-FEB-1994 (Rel. 28, Last annotation update) MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II LDL RECEPTOR I AND II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
                                          ROHRER L., FREEMAN M., KODAMA T., PENMAN M., "Coiled-coil fibrous domains mediate ligand l scavenger receptor type II.";
Nature 343:570-572(1990).
                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metartiodactyla; Ruminantia; Pecora; Bovo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                       "Type I macrophage scavenger receptor contains alpha-helical and collagen-like coiled coils.";
Nature 343:531-535(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
DOMAIN
                                                                                         TISSUE=LUNG;
MEDLINE; 90136973.
                                                                                                                 SEQUENCE
                                                                                                                                                                          KRIEGER M.;
                                                                                                                                                                                     KODAMA T., FREEMAN M.,
                                                                                                                                                                                                MEDLINE; 90136965
                                                                                                                                                                                                              TISSUE=LUNG
                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                              Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00134;
PROSITE; PS00135;
PROSITE; PS00420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                              394 PIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACY 433
                                                                                                                                                                                                                                                                                                                                                                                                                                     333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 IRLAGGKSTHEGRLEVYYKGQWGTVCDDGWTEMNTYVACRLLGFKYGKQSSVNHFDGSNR
FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS. TWO TYPES OF RECEPTOR SUBDUNITY EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING
                                                                                                                                                                                                                                                                                                                                                                                                                             PIWLDDVSCSGKEVSFIQCSRRQWGRHDCSHREDVGLTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
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21 POTENTIAL.
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TRYPSIN_SER; 1.
SPERACT_RECEPTOR; 3.
                                                                                                                 (SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%;
82.0%;
                                                                                                                                                                                                                       AND
                                                                                                                                                                                     ROHRER L.,
                                                                                                                                                                                                                       PARTIAL
                                                                                                              FORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 691; DB 1; I
Pred. No. 7.85e-157;
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CHARGE RELAY
CHARGE RELAY
POTENTIAL.
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3F3C4F35 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEUROTRYPSIN.
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                    ZABRECKY J.,
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RELAY SYSTEM.
RELAY SYSTEM.
RELAY SYSTEM.
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                                                                  KRIEGER M
                                                                                                                                                                                                                                                                                                       (MACROPHAGE ACETYLATED
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                                                                                                                                                                                     MATSUDAIRA
                                                                                                                                                                                                                                                          Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 761;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Signal
                                                                  macrophage
                                                                                                                                                                                                                                                         Bovidae;
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SULT

MSRE_HUMAN

MSRE_HUMAN

P21757; P21759;

T 01-MAY-1991 (Rel. 18, Created)

T 01-MAY-1991 (Rel. 18, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE MACROPHAGE SCAVENCER RECEPTOR TYPES I AND II

TOT RECEPTOR I AND II).
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MEDLINE; 91067661.
MATSUMOTO A., MAITO M., ITAKURA H., IKEMOTO S.,
HAYAKAWA I., KANAMORI H., ABURATANI H., TAKAKU
KOBARI Y., MIYAI T., TAKAHASHI K., COHEN E.H.,
                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa; (
Eutheria; Primates; (
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PIR; S08278; S08278.
PROSITE; PS00420; SPERACT_RECEPTOR; 1.
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                                                                                SEQUENCE FROM
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- SUBGUIT: HOMOTRIMER.
- SUBGELLULAR LOCATION: I
- ALTERNATIVE PRODUCTS: I
RECEPTOR (TYPES I AND I
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European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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OS -> PG (IN ISOFORM I
MISSING (IN ISOFORM II
M: 2CDE1EEL CRC32;
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EXTRACELLULAR (POTENTIAL).
SPACER (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413; DB 1;
No. 7.34e-81;
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                                                                                                                                        Vertebrata;
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MACROPHAGE SCAVENGER
BY ALTERNATIVE SPLICING
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                                       S., ASAOKA
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  F., SUZUKI H., WYDRO R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 453;
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MSRE_RABIT STANDARD; PRT; 005585; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence up 01-0CT-1996 (Rel. 34, Last annotation MACROPHAGE SCAVEMEER RECEPTOR TYPES ILDL RECEPTOR I AND II).

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Best Local
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EMBL; D90188; BAA14209.1;
PIR; A38415; A38415.
PIR; B38415; B38415.
MIM; 153622; -
                                                                                                                                                                                                                                                                                       PROSITE; PROUBLY, 1.
PRAM; PE00530; SRCR; 1.
PFAM; PF01391; Collagen; 1.
Transmembrane; Glycoprotein; Endocytosis; Coiled coil; LDL;
Transmembrane; Glycoprotein; Alternative splicing.
Heptad repeat pattern; Receptor; Alternative splicing.
CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOUSMAN D.E., KODAMA T.;

"Human macrophage scavenger receptors: primary structure, expression, and localization in atherosclerotic lesions.";

Proc. Natl. Acad. Sci. U.S.A. 87:9133-9137(1990).

-i- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS. TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIARE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING MODIFIED LOW DENSITY LIPOPROTEINS (LDL).
                                                                                                                                    VARSPLIC
SEQUENCE
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CARBOHYD
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 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF THE SAME GENE.
VRLVGGSGPHEGRVEILHSGQWGTICDDRWEVRVGQVVCRSLGYP-GVQAVHKAAHFGQG 408
                                                                                       Similarity
52; Conser
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49762
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                                                                                                                                     MW;
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ALPHA-HETICAL COILED-COIL.
COLLAGEN-LIKE.
CYS-RICH.
POTENTIAL.
                                                                                          18;
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Pred. No. 2.
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TPFTKVRLVGGSGP ->
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                                                                                       DB 1; Le
2.93e-79;
ches 28;
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BY ALTERNATIVE SPLICING
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Best Local Similarity
Matches 51; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Rabbit aortic smooth muscle cells express inducible macrophage scavenger receptor messenger RNA that is absent from endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                              EMBL; L11693; AAA31402.1; -.
EMBL; L11692; AAA31403.1; -.
EMBL; D13381; BAA02649.1; -.
PROSITE; PS00420; SPERACT_RECEPTOR;
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                                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOI T., WADA Y., KODAMA T., HIGASHI K.I., KURIHARA Y., MIYAZAKI T., NAKAMURA H., UESUGI S., IMANISHI T., KAWABE Y., ITAKURA H., YAZAKI Y., MATSUMOTO A.; "Charged collagen structure mediates the recognition of negatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                                                                                                                                                                                                                                                                                                                  Heptad repeat pattern;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGE
TWO TYPES OF RECEPTOR SUBURITS EXIST. THESE RECEPTORS MEDIAC
ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING
MODIFIED LOW DENSITY LIPOPROTEINS (LDL).
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PF01391; Collagen; 1
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                                                                                                                                                                                                                                                                                    Receptor: Alternative splicing.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ACCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                              W.
                              22;
                                          Score 405; DB 1;
Pred. No. 1.00e-78;
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POTENTIAL.
POTENTIAL.
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TPSATVR -> RPVOLTP (IN ISOFORM II).

MISSING (IN ISOFORM II).

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MACROPHAGE SCAVENGER
BY ALTERNATIVE SPLIC:
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                                                     Length
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                              Indels
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                                                                                                                                                                                                                                                                                                                            LDL;
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                              Gaps
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353 VRLVGGRGPHEGRVEILHNGQWGTVCDDHW-ELRAGQVVCRSLGYRGVKSVHKKAYFGQG 411

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MEDLINE: 9539538.

MEDLINE: 9539538.

MEDLINE: 9539538.

MEDLINE: 9539538.

"Structure of the murine macrophage scavenger receptor gene and evaluation of sequences that regulate expression in the macrophage cell line, p388D.";

J. Lipid Res. 36:1305-1314(1995).

"I- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS.

TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING ENDOCYTOSIS OF A DIVERSE RECEPTOR SUBUNITS EXIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Modentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger receptors.";
J. Biol. Chem. 268:2126-2133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE;
                                            This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JENKINS N.A., KRIEGER M.;
"An ancient, highly conserved revealed by cloning type I and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 349-458 MEDLINE; 91062370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOI T., WADA Y., KODAMA T., HIGASHI K.I., KURIHARA
MIYAZAKI T., NAKAMURA H., UESUGI S., IMANISHI T., I
ITAKURA H., YAZAKI Y., MATSUMOTO A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (SHORT MEDLINE; 93131972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structures and high and low affinity ligand binding properties murine type I and type II macrophage scavenger receptors."; J. Lipid Res. 34:983-1000(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-DEC-1999 (Rel. 39, Last annotation
MACROPHAGE SCAVENGER RECEPTOR TYPES I
                         between
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-4 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FREEMAN M., ASHKENAS J., REES D.J.,
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s SWISS-PROT entry is copyright. It is produ
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European Bioinformatics Institute. There a
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ALTERNATIVE PRODUCTS:
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                                                                                     OF THE SAME GENE
                                                                                                      RECEPTOR (TYPES I AND
                                                                                                                                                                        SUBUNIT:
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93359822.
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                                                                                                                                                                        HOMOTRIMER.
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THE TWO FORMS OF MACROPHAGE
II) ARE PRODUCED BY ALTERNAT
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 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.in-
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CARBOHYD
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SEQUENCE
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VARSPLIC
                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
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DOMAIN
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                                                                                                                                    WIJNGAARD P.L.J., METZELAAR M.J., MACHUGH N.D.,
                                                                                                                                                                                                                                                                                            WC11_BOVIN
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DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).

TRANSMEM 56 78 SIGNAL-ANCHOR (TYPE-II ME
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MGD; MGI:98257; SCVR
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                                                                                                      "Molecular characterization of the WC1 antigen on bovine CD4-CD8-gamma delta T lymphocytes.";
                                                                                                                                                  MEDLINE; 93056489.
                                                                                                                                                              TISSUE-BLOOD
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      ANTIGEN WC1
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                                                                                            bovine CD4-CD8-gamma delta T Immunol. 149:3273-3277(1992).
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L04275;
D13382;
M59445;
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Pred. No. 1.
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MISSING (IN ISOFORM II).
F28A456E CRC32;
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ALPHA-HELICAL COILED-COIL
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P30203;
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                                                                                                                                                                                                                                                                                                                    J. EXP. Med. 174:949-952(1991).

J. EXP. Med. 174:949-952(1991).

FUNCTION: INVOLVED IN CELL ADHESION. BINDS TO CD166-

I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: CONTAINS 3 SRCR DOMAINS.

DATABASE: NAME—PROW; NOTE—CD guide CD6 entry;

WWW—"http://www.ncbi.nlm.nih.gov/prow/cd/cd6.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                ARUFFO A., MELNICK M.B., LINSLEY P.S., SEED B.;
"The lymphocyte glycoprotein CD6 contains a repeated domain characteristic of a new family of cell surface and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence
15-DEC-1998 (Rel. 37, Last annotatio
T-CELL DIFFERENTIATION ANTIGEN CD6 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X63723; CAA45255.1;
PIR; S19913; S19913.
PIR; A46496; A46496.
                                                         CARBOHYD
                                                                                             DOMAIN
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                                                                                                                                         SIGNAL
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PFAM; PF00530; SRCR;
                                                                                                                 DOMAIN
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                        мім; 186720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELN-TYVVCRQLGFKYG-KQASANHFEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                931 LRLVDGGGPCGGRVEILDQGSWGTICDDDW-DLDDARVVCRQLGCGEALNATGSAHFGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 49.7%;
Local Similarity 47.5%;
                                                                                                                                                 adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGPIWLDDLNCTGKESHVWRCPSRGWGRHDCRHKEDAGVIC 1030
                                                                                                                                                                                                                x60992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
92013796.
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1436 AA;
                                                                                                                                                                                                                                                                        non-profit institutions as long
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S26741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                           SPERACT_RECEPTOR;
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 468
402
423
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468
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112
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333
345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154196 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 391; DB 1;
Pred No. 5.32e-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
POTENTIAL.
POTENTIAL.
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                                                                                          CYTOPLASMIC
                                                                                                                                                    Transmembrane;
                                                                                                                   EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D61545D7 CRC32;
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                                                                                                                 DIFFERENTIATION ANTIGEN ELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                    Repeat; Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (T12)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                    CARBOHYD
CARBOHYD
                                                                                                                                                                                                      REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                   the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MADDLINE: 89184581.

DANGOTT L.J., JORDAN J.E., BELLET R.A., GARBERS D.L.;

"Cloning of the mRNA for the protein that crosslinks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
11-AUG-1990 (Rel. 15, Last sequence upd
5-JUL-1999 (Rel. 38, Last annotation u
5-GG PEPTIDE SPERACT RECEPTOR PRECURSOR.
                                                                                                                                       SEQUENCE
                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; J04518; AAA30078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euechinoidea; Echinacea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strongylocentrotus purpuratus (Purple sea urchin) Eukaryota; Metazoa; Echinodermata; Echinozoa; Echi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPER_
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                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                       CHAIN
OMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                           Receptor;
                                                                                                                                                                                                                                                                                                                                          PFAM; PF00530; SRCR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                     PROSITE;
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        324
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                                                                                   Local Similarity
nes 45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: RECEPTOR FOR THE EGG PEPTIDE SPERACT SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :. Natl. Acad. Sci. U.S.A. 8
FUNCTION: RECEPTOR FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRLVDGGGACAGRVEMLEHGEWGSVCDDTW-DLEDAHVVCRQLGCGWAVQALPGLHFTPG 219
                                                                                                                                                                                                                                                                                                                                                                 A32751; A32751
      TWAPIHTSFVMCTGVEDRLIDCILRDGWT-HSCYHVEDASVVC 365
                                IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASANHFEE-S-
                                                  IRLMDGSGPHEGRVEIWHDDAWGTICDDGWDWADANVVCRQAGYRGAVKASGFKGEDFGF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTEL-NTYVVCRQLGFKYGKQA-SANHFEES 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGPIHRDQVNCSGAEA-YLWDCPGLP-GQHYCGHKEDAGVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
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                                                                                                                                                                                                                                                                                                                                                     PS00420;
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                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                      148
261
376
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115
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                                                                                    Conservative
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44.18;
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43.7%;
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                                                                                                                                       57820 MW;
                                                                                                                                                                                                                                                                                                                         Glycoprotein; Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 293; DB 1;
Pred. No. 2.22e-49;
                                                                                    19;
                                                                                                 Score 281; DB 1;
Pred. No. 2.60e-46;
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                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86:2128-2132(1989)
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                                                                                                                                                                                                                                           YTOPLASMIC (POTENTIAL)
X APPROXIMATE TANDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  042D5AC8
                                                                                                                                       D27174AE CRC32;
                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                 PEPTIDE SPERACT RECEPTOR
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                                                                                                                                                                                                                                               TANDEM REPEATS
                                                                                    34;
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                                                                                                          Length 532;
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                                                                                   Indels
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P19238;
PNTK_FIG STANDARD; PRT; 1034 AA.
p98074;
p198074;
p198074;
p1996 (Rel. 33, Created)
p1-FEB-1996 (Rel. 33, Last sequence update)
p15-JUL-1998 (Rel. 36, Last annotation update)
p15-JUL-1998 (Rel. 36, Last annotation update)
p15-JUL-1998 (Rel. 36, Last annotation update)
p15-JUL-1998 (Rel. 36, Last annotation update)
p15-JUL-1998 (Rel. 36, Last annotation update)
p17-JUL-1998 (Rel. 37, Last annotation update)
p18-JUL-1998 (Rel. 37, Last annotation update)
p18-JUL-1998 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extrement by the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 18:5296-5296(1990).
-!- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING PROLIFERATION. CD5 INTERACTS WITH CD72/LYB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR (LYMPHOCYTE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Transmembrane; SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X53061; PIR; S11270; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD5
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS 2 SRCR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T1/LEU-1) (LYMPHOCYTE ANTIGEN CD5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                           334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                             34 MRLSGSGSRCQGRLEVSNGTEWYAVHSQSWGQLSLYQVAPRQF
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                                                                                                                                                                                           IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTY-VVCRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00530;
                                                                                                                                                                                                                                                                    h 14.5%;
Similarity 37.2%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1270; S11270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Bovine).
Metazoa; Chordata; Craniata; Vertebrata; Mamme
Metartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA37231.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRCR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                      495
134
382
108
151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; T-cell
                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                      Score 114; DB 1;
Pred. No. 4.72e-07;
                                                                                                                                                                                                                                                                                                                                                POTENTIAL. ; F8ED2AE0
                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SURFACE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                  CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS00740; MAM_1; 1.

PROSITE; PS50060; MAM_2; 1.

PROSITE; PS50068; LDLRA_2; 2.

PROSITE; PS01209; LDLRA_2; 2.

PROSITE; PS01068; LDLRA_2; 2.

PROSITE; PS01068; LDLRA_2; 2.

PFAM; PF00057; 1dl_recept_a; 2.

PFAM; PF00089; tryPsin; 1.

PFAM; PF00089; tryPsin; 1.

PFAM; PF00089; tryPsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - SUBUNIT: HETEROTRIMEN OF A CHILL (HEAVY) CHAIN, AND A MINI CHAIN.
- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROTEIN THE CHAINS ARE DERIVED FROM A SINGLE PRECURSO:
- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSO:
- PTM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.
- SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAIN:
- SIMILARITY: CONTAINS 2 CUB DOMAINS.
- SIMILARITY: CONTAINS 1 SACR DOMAIN.
- SIMILARITY: CONTAINS 1 SACR DOMAINS.
- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO
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"Structural characterization of porcine enteropeptidase.";
"5 Biol. Chem. 269:19976-19982(1994).
"1- FUNCTION: RESPONSIBLE FOR INTIATING ACTIVATION OF PANCREATIC PROTECLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPT.
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
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PF01390;
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HERZENBERG L.A., STROMINGER
"Isolation of complementary
glycoprotein T1/Leu-1.";
         VAN DE VELDE H., VON HOEGEN I., LUO W., PARNES J.R "The B.cell surface protein CD72/Lyb-2 is the 11ga Nature 351:662-665(1991).
-i- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING
                                                                                                                                                                                    Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 87014786.
                                                                                                                                                                          Eutheria; Primates;
                                                                                     Nature 323:346-349(1986).
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Best Local S
Matches 1
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015393;
15-JUL-1998
15-JUL-1998
15-JUL-1998
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CARBOHYD
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DISULFID
                                                                                      the
                                                                                                                                                                                                                              Genomics 44:309-320(1997).

-:- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
-:- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN SMALL INTESTI
WEAKLY IN SEVERAL OTHER TISSUES.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                    PAOLONI-GIACOBINO A., CHEN H.
ANTONARAKIS S.E.;
"Cloning of the TMPRSS2 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
MEDLINE; 97468144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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MIM; 153340; -.
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DATABASE: NAME=PROW; NOTE=CD guide CD5 entry;
                                                                                  European Bioinformatics Institute.
                                                                                                                                                                     SIMILARITY: CONTAINS SIMILARITY: CONTAINS
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                                                                                                                                                                                                               TRYPSIN FAMILY
                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration -
en the Swiss Institute of Bioinformatics and the EMBL outstation -
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Similarity 37.9%;
11; Conservative
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Catarrhini; Hominida
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LDL-RECEPTOR CLASS A DOMAIN.
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Pred. No. 2.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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titute. There are no rest
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2.72e-05;
2.3e-9;
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01-NOV-1997 (Rel. 3
15-JUL-1998 (Rel. 3
ENTEROPEPTIDASE (EC
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01-NOV-1997
15-JUL-1998
                                                                                                                      YUAN X., LU D., RUBIN D.C., PUNG C.Y.M., SADLER J.E.;
SUBMITTED (DEC-1996) to the EMBL/GenBank/DDBJ databases.

-i- function: responsible for initiating activation of pancreatic protectific proenzymes (Trypsin, Chymotrypsin and Carboxypeptidase A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN, PROCARBOXYPEPTIDASES, AND PROENZYMES (BY SINLIARITY).

-i- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
   ----
                                                                                                                                                                                                                                            Mus musculus (Mouse)
Eukaryota; Metazoa;
Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                    ENTK_MOUSE P97435;
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PROSITE;
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HSSP;
                                                                                                                                                                                                             STRAIN-C57BL/6;
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                                                                                                                                                                                                                                                                                                                                                                                                              165 RKSWHPVCQDDWNENYGRAACRDMGYK 191
PIM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSO! CLEAVED BY A TRYPSIN-LIKE PROTEASE (BY SIMILARITY) SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAIN. SIMILARITY: CONTAINS 2 CUB DOMAIN. SIMILARITY: CONTAINS 1 SRCR DOMAIN. SIMILARITY: CONTAINS 1 MAM DOMAIN.
                                                                  SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE)
                                                                                        SUBUNIT: HET
                                                                                                              TRYPSINOGEN
                                                                                SIMILARITY)
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11; Conser
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                                                                                        HETERODIMER OF A AIN (HEAVY) CHAIN
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el. 35, Last sequ
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40.7%;
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150
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Sciurognathi;
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Last annotation update)
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Pred. No. 2.40e-04
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                                                                                        (LIGHT) CHAIN AND A DISULFIDE BOND
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HSSP; P00763;
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PF00530; SRCR; 1.
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PS50060;
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; LDLRA_1; 2.
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CHARGE RELAY SYSTEM
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NON-CARLYTIC CHAIN (HEAVY CHAIN).

CATALYTIC CHAIN (LIGHT CHAIN).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

LDL-RECEPTOR CLASS A 1.
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P98073;
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modified and this statement is not remov-
entities requires a license agreement (so
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Enterokinase, the initiator of intestinal digestion, is a mosaic protease composed of a distinctive assortment of domains.";

Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).
-!- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC PROTEOLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCUDING CHYMOTRYPSINOGEN, PROCARBOXYPEPTIDASES, AND PROELASTASES.
-!- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "cDNA sequence and chromosomal localization the proteolytic activator of trypsinogen."; Biochemistry 34:4562-4568(1995).
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KITAMOTO Y., YUAN X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KITAMOTO Y., VEILE R.A., DONIS-KELLER H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER OF A CATALYTIC (LIGHT) CHAIN AND A MULTIDOMAIN (HEAVY) CHAIN LINKED BY A DISULFIDE BOND. SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE). TISSUE SPECIFICITY: INTESTINAL BRUSH BORDER. PIM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
                                                                                                                                                                                                                                                                                                                                                             MALABSORPTION CHARACTERIZED BY DIARRHEA AND FAILURE SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS. SIMILARITY: CONTAINS 2 CUB DOMAIN. SIMILARITY: CONTAINS 1 SRCR DOMAIN. SIMILARITY: CONTAINS 1 SRCR DOMAIN. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNG SIMILARITY S1; ALSO KNG SIMILARITY S1; ALSO KNG SIMILARITY S1; ALSO KNG SIMILARITY S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; ALSO KNG S1; A
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DISEASE: DEFECTS IN PRSS7 CAUSE LIFE-THREATENING INTESTINAL
                                                                                                                                                                                                                                                                                                                                           TRYPSIN FAMILY.
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TRYPSIN_HIS; TRYPSIN_SER;
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Use lists 2003

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dd_ų protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:30:49 2000; MasPar time 16.65 Seconds 416.315 Million cell updates/sec

Description: Perfect Score: Title: >US-09-147-947-6 (334-433) from US09147947A.pep (5 of 6) 787

Sequence: 1 IRLAGGKGSHEGRLEVYYRG.....RRQWGRHDCSHREDVSIACY 100

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 7:sp_mhc 8:sp_organelle
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 37.816; Variance 60.520; scale 0.625

SUMMARIES

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
412 412 412 412 412 412 383 383 383 364 365 365 366 366 366	Score
5523.5 55	% Query Match
2043 918 11149 11149 11156 1155 2153 369 2153 369 7746 600 1594 4622 4622 4625 1785 1785 1785 1785	% Query Match Length
133 131 131 131 131 131 131 131 131 131	DB
096943 092098 007898 007991 007899 007899 0079375 029110 0974K0 029111 028910 029111 028810 0298810	ID
SRCR DOMAIN, MEMBRANE PEMA-SRCR PROTEIN PREC M130 ANTIGEN, EXTRACEL M130 ANTIGEN, CYTOPLAS M130 ANTIGEN, CYTOPLAS SCAVENCER RECEPTOR CYS SCAVENCER-RECEPTOR PRO LYSYL OXIDASE-RELATED SCAVENCER-RECEPTOR PRO MUCIN (FRAGMENT). HENSIN. MEMBRANE PROTEIN SCAVE PANCREAS CANCER-ASSOCI MAC-2 SIDDING PROTEIN LYSYL OXIDASE RELATED DMET1/6KB.1 PROTEIN PR DMET1/FROTEIN. MEMBRANE	Description
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CEGE.	C ブルブ	CD6C.	CD6E.	LYSYL OXIDASE-LIKE PRO	LYSYL OXIDASE HOMOLOG	SP85.	SCAVENGER RECEPTOR CYS	M130 ANTIGEN (FRAGMENT	SCAVENGER-RECEPTOR PRO	LYSYL OXIDASE-RELATED	UNKNOWN MRNA, PARTIAL	SCAVENGER-RECEPTOR PRO	SCAVENGER-RECEPTOR PRO	CYCLOPHILIN C-ASSOCIAT	MACROPHAGE RECEPTOR MA	SP ALPHA.	MUCIN (FRAGMENT).		CRP-DUCTIN PRECURSOR (PEPTIDYLPROLYL ISOMERA	EBNERIN.	BACTERIA BINDING MACRO	SP-ALPHA.	SP-ALPHA.	
1.0/e-40	_	4	1.57e-45	5.83e-4	.36e-4	.10e-4	.10e-	1.63e-5	.37e-5	.92e-	5	.19e-	.81e-5	1.37e-56	.37e-5	1.47e-5	.74e-	.57e-5	.92e-5	.92e-5	.66e-	.50e-	5.42e-6		

ALIGNMENTS

RES ID AC DT DT	Qy Db	z m O	ACC OCC OCC OCC OCC OCC OCC OCC OCC OCC
PRESULT 2 ID 092098 PRELIMINARY; PRT; 918 AA. AC 092098; DT 01-NOV-1996 (TIEMBLIEL 01, Created) DT 01-NOV-1996 (TIEMBLIEL 01, Last sequence update) DT 01-NOV-1999 (TIEMBLIEL 12, Last annotation update)	936 IRLVGGSGPHEGRVEIYYQGVWGTVCDDSWGQPDADVVCRQLGYANASRATVRAEFGRGT 995	Query Match 54.9%; Score 432; DB 5; Length 2043; Best Local Similarity 51.0%; Pred. No. 1.87e-79; Matches 51; Conservative 21; Mismatches 27; Indels 1; Gaps 1;	ID 099943; PRELIMINARY; PRT; 2043 AA. 477 AC 096943; AC 096943; DT 01-MAY-1999 (TIEMBLrel. 10, Created) DT 01-MAY-1999 (TIEMBLrel. 11, Last sequence update) DT 01-NOV-1999 (TIEMBLrel. 12, Last annotation update) DE SRCR DOMAIN, MEMBRANE FORM 2. GN SECRM 2. GN Geodia cydonium (Sponge). CC ELKARYOta; Metazoa; Porifera; Demospongiae; Tetractinomorpha; CC ELKARYOta; Metazoa; Porifera; Demospongiae; Tetractinomorpha; CC Astrophorida; Geodiidae; Geodia. RN [1] RP SEQUENCE FROM N.A. RN MEDLINE; 98369606. RN MEDLINE; 98369606. RN MEDLINE; 98369606. RN MUELLER I., MUELLER W.E.G.; RA MUELLER I., MUELLER W.E.G.; RA MUELLER I., MUELLER W.E.G.; RA MUELLER I., MUELLER W.E.G.; RA "The putative sponge aggragation receptor. Isolation and characterization of a moleCule composed of scavenger receptor cysteine-rich domains and short consensus repeats."; J. Cell Sci. 111:2635-2644(1998). DR HSSE; P10998; IVVC. DR PROSITE; PS00420; SPERACT_RECEPTOR; 8. PROSITE; PS00420; SPERACT_RECEPTOR; 8. SCQUENCE 2043 AA; 220896 MW; 4CE19401 CRC32;

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RITTER M., BÜECHLER C., LANGMANN T., SCHMITZ G.;

"Genomic organization of the human CD163 gene.";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ dat

EMBL; 722968; CA840541.1;

EMBL; 718388; CA845233.1;

FEMBL; 718399; CA845233.1;

FEMBL; 718399; CA845233.1;

FEMBL; 718391; CA845233.1;

FEMBL; 718392; CA845233.1;

FEMBL; 718392; CA845233.1;

FEMBL; 718393; CA845233.1;

FEMBL; 718394; CA845233.1;

FEMBL; 718396; CA845233.1;

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"A CDNA clone from the sea lamprey Pe scavenger receptor Cys-rich (SRCR) dc Gene 164:267-271(1995).

EMBL; U20652; AAA90990.1; -.
HSSP; P08709; 1BF9.
PFAM; PF000008; EGF; 4.
PFAM; PF00530; SRCR; 2.
PFAM; PF00100; zona_pellucida; 1.
                                                                                                                                                                                                                                                                                                                      LAW S.A., MICKLESS ....

AASON D.Y.;

"A new macrophage differentiation antigen scavenger receptor superfamily.";

Scavenger receptor superfamily.";

To Immunol. 23:2320-2325(1993)
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Q07898;
01-NOV-1996
01-NOV-1999
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M130 ANTIGEN
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RITTER M., BUECHLER C.,
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Eukaryota; Metazoa; Chordata; Craniata; Cephalaspidomorphi;
Petromyzontiformes; Petromyzontidae; Petromyzon.
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Pred. No. 3.17e-76;
21; Mismatches 25;
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O1-NOV-1999 (TIEMBLREL. 12, Last sec
O1-NOV-1999 (TIEMBLREL. 12, Last sec
M130 ANTIGEN CYTOPLASMIC VARIANT 1
HOMO Sapiens (Human)
Eukaryotta, Metazoa; Chordata; Crania
Eutheria; Primates; Catarrhini; Homi
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EMBL; Y18401; CAB45233.1; J
EMBL; Y18402; CAB45233.1; J
EMBL; Y18403; CAB45233.1; J
EMBL; Y18403; CAB45233.1; J
PFAM; PF00530; SRCR; 9.
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01-NOV-1996
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Eukaryota; Metazoa; Chordata
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Antigen; Signal.
1 40 F
                                                                                                                                                                                                                                                                                 SIGNAL
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Eur. J. Immunol. 23:2320-2325(1993).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                    PRINTS; PR00258; SPERACTRCPTR.
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Similarity 48.5%;
49; Conservative •
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Similarity 48.5%;
49; Conservative
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 Primates; Catarrhini; Hominidae; Homo.
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49 M130 ANTIGEN,
124328 MW; 4901C708
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VARIANT 1 PRECURSO
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VARIANT PRECURSOR.
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Pred. No. 1.72e-74;
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097375;
01-MAY-1999
01-MAY-1999
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                                                                                                                                                                                                                              SIGNAL
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                                  097375
                                                                                                                                                                                                                                                            PRINTS; PR00258; SPERACTRCPTR.
                                                                                                                                                                                                                                                                                                scavenger receptor superfamily.";
Eur. J. Immunol. 23:2320-2325(1993).
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Eur. J. Immunol. 23:2320-2325(1993).
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SEQUENCE FROM N.A.
MEDLINE; 93380506.
LAW S.A., MICKLEM K.J.,
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                                                                                                                                                                                                                                                                                                               "A new macrophage differentiation antigen scavenger recentor superfamily.";
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                                                                             392 TGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                                                                                                                               714 LRLVNGGGRCAGRVEIYHEGSWGTICDDSW-DLSDAHVVCRQLGCGEAINATGSAHFGEG 772
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Pred. No. 1.72e-74;
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M130 ANTIGEN,
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Pred. No. 1.72e-74;
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M130 ANTIGEN, CYTOPLASMIC
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SEQUENCE
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Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
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SIGNAL 1
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EMBL; AF064259; AAD08654.1 --
PROSITE; PS00420; SPERACT_RECEPTOR; 15.
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                                                                                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                Immunogenetics 46:276-282(1997).
EMBL; X99333; CAA67707.1; -.
    391
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                                            93
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                                                                                                                                   LRLVDG-GSYCSGSVEILHQGSWGTVCDDSW-DLDDAHVVCRQLGCGKTLSALGSAHFGA 92
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STGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC
                                          GSGRIWLDDVNCTGKESHLWQCPSRGWGQHNCRHKEDAGVIC 134
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                                                                                         IRLAGGKGSH-EGRLEVYYRGQWGTVCDDGWTELN-TYVVCRQLG-FKYGKQASANHFEE 390
                                                                                                                                                                                                                                                                                                                                          PF00530;
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Similarity 48.0%;
49; Conservative
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Similarity 48.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cetartiodactyla;
                                                                                                                                                                                                                                                                         369
369 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata; Craniata; Vertebrata;
Jetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 (TrEMBLIEL. 01, 05 (TrEMBLIEL. 01, 01, 01) (TrEMBLIEL. 12, 02) (TrEMBLIEL. 12, 03)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2153 AA;
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                                                                                                                                                                                                                                                                                                                                        SRCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
2153
                                                                                                                                                                                                                                                                                                                                                                SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                         369
39710 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAVIDSON E.H.;
numune System: Transcription
ian Immune System Expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
(FRAGMENT).
                                                                                                                                                                                              Score 383; DB 6;
Pred. No. 2.46e-67;
                                                                                                                                                                                Pred.
23; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
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Pred. No. 1.72e-74;
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SCAVENGER RECEPTOR CYSTEINE-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                         C669BB4B CRC32;
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                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      scavenger-receptor
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in Sea Urchin
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Q29111
Q29111;
Q29111;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Q1-NOV-1998 (TREMBLREL. 08, Last annotation update)
Q1-NOV-1998 (TREMBLREL. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
SIGNAL
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SEQUENCE
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Mechanisms for variability in a
cysteine-rich superfamily.";
Immunogenetics 46:276-282(1997).
EMBL; X99334; CAA67708.1; -.
PFAM; PF00530; SRCR; 5.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-NOV-1999 (TrEMBLrel. 12, Last annotation
LYSYL OXIDASE-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAITO
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Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WS9-14.
Homo sapiens (Human).
Chordata; Craniata;
Hominida
                                                                                                430
                                                                                                                                                      392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 EGPIWLDNLHCTGNEATLAACTSNGWGVTDCKHTEDVGVVC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334
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                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 48.7%;
Local Similarity 47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRLAGQKRKHSEGRVEVYYDGQWGTVCDDDFSIHAAHVVCRELGYVEAKSWTASSSYGKG
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                                                                                                SGRIWLDDVNCTGKESHLWQCPFRGWGRHDCRHKEDAGVIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC
                                                                                                                                                                                                                                                                                                    h 48.3%;
Similarity 46.5%;
47; Conservative
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on of a Novel Gene Encoding a Lysyl Oxidase-Related
ar Adhesion and Senescence.";
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23
546
546 AA;
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546
                                                                                                                                                                                                                                                                                                                                                                                                                                                59112 MW;
                                                                                                                                                                                                                                                                                                    Score 380; DB 6; Lo
Pred. No. 1.34e-56;
25; Mismatches 26;
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Pred. No. 2.46e-67;
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Best Local S
Matches 4
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Best Local Similarity 50.5%;
Matches 51; Conservative
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Q28910;
01-NOV-1996 (TIEMBLIEL 0
01-NOV-1996 (TIEMBLIEL 0
01-NOV-1998 (TIEMBLIEL 0
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Q95218 PREL
Q95218; Q95219;
Q1-FEB-1997 (TrE
Q1-MAY-1999 (TrE
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00420; SPERACT_RECEPTOR; 6. PFAM; PF00530; SRCR; 2. SEQUENCE 1594 AA; 172763 MW; 34EBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Hensin, a new collecting duct protein involved plasticity of intercalated cell polarity."; J. Clin. Invest. 98:2324-2331(1996).
EMBL; AF043112; AAD02242.1; -.
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MEDLINE; 97096804.
TAKITO J., HIKITA C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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EMBL; S78981; AAB35069.1; -.
PFAM; PF00530; SRCR; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HENSIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 95374471.
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       393
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                                                                                                                                                                               VRLVNGSTRCQGRVEVLYRGSWGTVCDDSWDINDASVVCRQLGCGWAVSAPGSARFGQGS
   GPIWLDDVSCSGKETRFL-QCSRRQWGRHDCSHREDVSIAC
                                                                     GSIFLDEVSCSGQEP-YLWNCSHRGWLSHNCGHYEDAGVIC
                                                                                                                                           IRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYG-KQASANHFEEST
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                                                                                                                                                                                                                                                                                      Similarity 47; Conser
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63999 MW;
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                                                                                                                                                                                                                                                                              Score 369; DB 6;
Pred. No. 6.69e-64;
22; Mismatches 29
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Pred. No. 3.99e-65;
19; Mismatches 28
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Best Local :
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Submitted (OCT-1996) to the EMBL/GenB
EMBL, U73375, AABL8745.1; -
PROSITE; PS00420; SPERACT_RECEPTOR; 1
PFAM; PF00530; SRCR; 1.
PRINTS; PR00258; SPERACTRCPTR.
SEQUENCE 578 AA; 64398 MW; 002E8BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P70117
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MEDILINE; 95169648.

O'KEEFFE M.A., METCALFE S.A., GLEW M.D., BOWDEN T.,

KIMPTON W.G., CAHILL R.N., HEIN W.R., WALKER I.D.;

"Lymph node homing cells biologically enriched for express multiple genes from the T19 repertoire.";

Int. Immunol. 6:1687-1697(1994).

EMBL; S76311; AAB33543.1;

EMBL; S76313; AAB33543.1;

EMBL; S76311; AAB33543.1;

EMBL; S76311; AAB33543.1;

CREANT DECEMBER.
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Q28881
Q28881;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat)
PANCREAS CANCER-ASSOCIATED PROTEIN 4.
                                                                                                                                                                                                                                                                                                                                               Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocr
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MEMBRANE PROTEIN SCAVENGER RECEPTOR HOMOLOG (FRAGMENT).
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Local Similarity 43.6%;
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                                                                                 MRLVNGASANEGRVEIFYRGQWGTVCDNLWNILDANVVCRALGYENATQALGRAAFGPGR 83
 GPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC 432
                                 GPVMLDEVECTGTEPSLANCSSLGWLKSRCGHEKDAGVVC
                                                              | IRLAGGKGSHEGRLEVYYRGQMGTVCDDGWTELNTYVVCRQLGFKYGKQA-SANHFEEST 392
                                                                                                                                    Similarity 43; Conser
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llarity 43.0%;
Conservative
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                                                                                                                                Score 364; DB 11;
Pred. No. 1.12e-62;
22; Mismatches 34;
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Pred. No. 6.38e-63;
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J. Biol. Chem. 268:14245-14249/1902\
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EMBL; X79089; CAA55699.1;
PFAM; PF00530; SRCR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ULLRICH A., SURES I., D'EGIDO M., JALLAL B., DREPS A., AZAM M., RUBINSTEIN M., NATOLI C.; "The secreted tumor-associated antigen 90K is
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                   GPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC
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Similarity 43.0%;
43; Conservation
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585 MAC-2 BINDING PRO
65330 MW; AAEA9E32 CRC32;
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h_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 13 10:35:21 2000; MasPar time 4.74 Seconds 276.325 Million cell updates/sec

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Description: Perfect Score: >US-09-147-947-6 (447-547) from US09147947A.pep (6 of 6) 757

1 VRLMDGENKKEGRVEVFING.....KQDIGRHNCRHSEDAGVICD 101

Scoring table: PAM 150 Gap 11 Sequence:

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics: a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Mean 26.647; Variance 104.824; scale 0.254

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Applicati 6.8 Applicati 6.8 Applicati 6.8 Applicati 1.3 Applicati 2.4 Applicati 2.4 Applicati 2.6 Applicati 2.6 Applicati 3.6 Applicati 8.8 Applicati 8.8 Applicati 8.8 Applicati 8.8 Applicati 8.8 Applicati 8.8 Applicati 8.8 Applicati 8.8 Applicati 1.3 Applicati 3.6
pplicati 6.80e 3 pplicati 6.80e 3 pplicati 1.31e 2 plicatio 2.46e 2 plicatio 2.68e 2 plicatio 1.31e 2 plicatio 8.84e 2 plicatio 8.84e 2 plicatio 8.84e 2 plicatio 1.21e 2 plicatio 3.61e 2 plicatio 3.61e 2 plicatio 2.39e 0 plicatio 2.39e 0 plicatio 2.39e 0 plicatio 2.39e 0 plicatio 2.39e 0 plicatio 2.39e 0 plicatio 2.39e 0 plicatio 2.39e 0
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ALIGNMENTS

8888888	888888888888888888	88888888888888	RESULT ID U XX ACC X ACC X XX DT DT XX XX
	etille chace	Sequence 10, Application US/08316714 Patent No. 3965382 GENERAL INFORMATION: APPLICANT: Koths, Kirston E. APPLICANT: Halenbeck, Robert F. APPLICANT: Taylor, Eric w. APPLICANT: Wang, Alice M. APPLICANT: Casipit, Clayton L. TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprote NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSEE: Cetus Oncology Corporation STREET: 1400 Fifty-Third Street CITY: Emeryville STATE: CA	LT 1 US-08-316-714-10 STANDARD; PRT; 585 AA. xxxxxx Sequence 10, Application US/08316714

CORRESPONDENCE ADDRESS: ADDRESSED: Cetus Oncology Corporation STREET: 1400 Fifty-Third Street CITY: Emeryville STATE: CA	TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein	APPLICANT: Casipit, Clayton L.	APPLICANT: Wang, Alice M.	APPLICANT: Taylor, Eric W.	APPLICANT: Halenbeck, Robert F.	APPLICANT: Koths, Kirston E.	GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:

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                                           NAME: Goldman, Kenuera 24,174
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 2595.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 420-3152
TELEFAX: (510) 658-5470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08477674 Patent No. 5644035
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                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                           FILING DATE:
APPLICATION NUMBER: US/07
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Koths, Kirston E.
APPLICANT: Halenbeck, Robert F.
APPLICANT: Taylor, Eric W.
APPLICANT: Wang, Alice M.
APPLICANT: Casipit, Clayton L.
TITLE OF INVENTION: Secreted Mac-2-Binding Glycoprotein
                                                                                                                                                                                        PRIOR APPLICATION DATA:
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JENCE 585 AA; 65330 MW; 1874129 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546
                                                                                                                                                                                                   FILING DATE: 07-JUN
CLASSIFICATION: 530
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TOPOLOGY: 11
                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                             CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Cetus Oncology Corporation STREET: 1400 Fifty-Third Street
                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                              ZIP: 94608
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                                                                                                                                                                                                                            US/08/477,674
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Pred. No. 6.80e-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08473791
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les 52; Conservativa
                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 585 amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
UENCE 585 AA; 65330 MW; 1874129 CN;
                                                                                                                                              FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (510) 420-3152
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TITLE OF INVENTION: Secreted Mac-2-Binding.Glycoprotein
 MOLECULE TYPE:
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        TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
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                                                                        TELEPHONE: (510) 658-5470
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CITY: Emeryville
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                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                 REFERENCE/DOCKET NUMBER: 2595.1
                                                                                                                         NAME: Goldman, Kenneth REGISTRATION NUMBER: 34
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1400 Fifty-Third Street
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Pred. No. 6.80e-30;
17; Mismatches 31
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APPLICANT: KREIGER, MONTY; KODAMA, TATSUHIKO
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                                                                      Sequence 7, Application US/08794795 Patent No. 5916766
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nes 49; Consen
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                                                          GENERAL INFORMATION:
    APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 16-SEP-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 391,486
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: 272,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/307,400
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52; Conser
    CANT: Adamou, John
CANT: Gross, Mitchell
CANT: Lysko, Paul
OF INVENTION: Human N
                                                                                                                                                                                                                                                                                                                                                     491 AA;
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ilarity 52.0%;
Conservative
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                                               Elshourlagy, Nabil
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    Human Macro
                                                                                                                                                                                                                                                                                                        Score 376; DB 4; Le
Pred. No. 2.46e-28;
17; Mismatches 34;
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Pred. No. 6.80e-30;
17; Mismatches 31;
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    Scavenger
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Best Local :
APPLICANT: Kangas, N
TITLE OF INVENTION:
Patent NO. 5691197
TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                           Sequence 2, Application Patent No. 5691197
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                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatibl OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for VCURRENT APPLICATION DATA:
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ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
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Similarity 54.0%;
54; Conservative
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04-FEB-1997
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An Insolated DNA Sequence For a
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a Collagenous Domain and the
Polypeptide Chain Encoded by
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Pred. No. 1.31e-27;
17; Mismatches 24
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                                                                                                                                                                                                                                                                                                                                                                423 VRIMGGTNR--GRAEVYYNNEWGTICDDDWDNNDATVFCRMLGY---SRGRALSSYGGGS 477
                                                            APPLICANT: Resnick, David
APPLICANT: Kreiger, Monty
APPLICANT: Joiner, Keith A.
TITLE OF INVENTION: Method for TI
TITLE OF INVENTION: Septicemia
NUMBER OF SEQUENCES: 2
                                                                                                                              GENERAL INFORMATION:
APPLICANT: Dunne, Dana W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: (216) 980162
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PS/2, Mode
OPERATING SYSTEM: DOS 5.
SOFTWARE: WORD PERFECT 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEPAX: (216) 241-1666
                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Minnich, Richard J
                                                                                                                                                                                                                                                                                                            GNIWLDNVNCRGTENSLWDCSKNSWGNHNCVHNEDAGVEC 517
                                                                                                                                                                                                                                                                                                                                        VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                                                                                                                                                                                                                                                               GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546
                   STREET:
                    ADDRESSEE: Patrea L. raus-
STREET: 1100 Peachtree Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 518 amino aci
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1100 Superior Avenue STREET: Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear
CE 518 AA; 52730 MW; 1281000 CN;
                                                                                                                                                                                                                                                                                                                                                                                    h 48.7%;
Similarity 54.0%;
54; Conservative
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E: Ohio
                  Atlanta
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           Ga
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Pred. No. 1.31e-27;
17; Mismatches 24;
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                                                                                   Treating Gram-Positive
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RESULT 8
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Best Local Similarity 49.0%;
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                                                                                                                                                                                                                                                                              410 GPIWLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTC 449
                                                                                                                       Sequence 2, Application US/08453117 Patent No. 5683903
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                                                                                                                                                                                                                                                                                                            447 VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                                                                GENERAL INFORMATION: APPLICANT: Lysko,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO:
                                          APPLICANT: Brawner, Mary E.
TITLE OF INVENTION: Attachment Enhanced
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (404)-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546
                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES: 905 -
STREET: Mailcode - UW2220, CITY: King of Prussia
                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                 RELEVANT RESIDUES IN SEQ ID NO: 1
ICE 451 AA; 49841 MW; 1025052 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                          VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS: Ashkenas, et al. JOURNAL: J. Lipid Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                     Lysko, Paul G.
Elshourbagy, Nabil A.
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                     U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo sapien
                                SmithKline Beecham - Corporate Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal
                                                                                                                                                                                                                       STANDARD;
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Pred. No. 2.68e-27;
17; Mismatches 34
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            Swedeland
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                                                                 293 Cells
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ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS

STATE: P

Pennsylvania .: U.S.A.

SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,117 FILING DATE:

TELEFAX: (610) 270-50: INFORMATION FOR SEQ ID NO:

270-5090

2

TELEPHONE: (610) 270-5019

REGISTRATION NUMBER: 31 REFERENCE/DOCKET NUMBER:

SBC-P50338

Jervis, Herbert H.

ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

435

ATTORNEY/AGENT INFORMATION:

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Best Local Similarity 49.0%;
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08973145 Patent No. 5919636
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                      ZIP: 19406-5090

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                    SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein JENCE 451 AA; 49762 MW; 1024670 CN;
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                 APPLICANT: Elshourbagy, Nabil A.
APPLICANT: Brawner, Mary E.
                                                                                                                                                                                                                                                                                APPLICANT: Lysko, Paul G
                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                       TITLE OF INVENTION: Attachment Enhanced 293 Cells
                                                                                                                                                 ADDRESSEE: Smithkline Beecham - Corporate Patents U.S. STREET: Mailcode - UW2220, 709 Swedeland Road CITY: King of Prussia STATE: Pennsylvania
          APPLICATION NUMBER: US/0 FILING DATE: 26-NOV-1997
CLASSIFICATION:
                                                                                                                                       COUNTRY:
                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                         US/08/973,145
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Pred. No. 8.84e-27;
17; Mismatches 34
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                                                    Version
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Best Local 9
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 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9608081
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9608081 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                                      TELEPHONE: (610) 270-
TELEFAX: (610) 270-50
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 47.7%;
Local Similarity 49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (610) 270-5090 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P50338
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Attachment Enhanced 293 Cell's
NUMBER OF SEQUENCES: 4
                                  SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
JENCE 451 AA; 49762 MW; 1024670 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: P-41, 8
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
MOLECULE TYPE: ENCE 451 AA;
                                                                                            TELEPHONE: (610) 270-5019
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 451 amino acids
                         TOPOLOGY:
                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                  CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                            APPLICATION NUMBER: PCT/US96/08081
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                                                                                                                                                                                                                                                                                                       Pennsylvania
                                                                                                                                                                                                                                                                                                                              E: SmithKline Beecham - Corporate Patents U.S. Mailcode - UW2220, 709 Swedeland Road
                         linear
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49762 MW;
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270-$090
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  1024670 CN;
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Length 451;

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Best Local
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447 VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
              350 VRLVGGSGPHEGRVEILHSGQWGTICDDRWEVRVGQVVCRSLGYPGVQAVHKAAHFGQGT 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                    Local Similarity hes 49; Conser
                                                                                                                                                              TELEFAX: (610) 270-5090 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Lysko,
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5019
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/948,222
                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Brawner, Mary E.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPIWLNEVFCFGRESSIEECKIRQWGTRACSHSEDAGVTC 449
                                                                                                                           TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       NAME: Jervis, Herbert REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: SmithKline Beecham - Corporate Patents ADDRESSEE: U.S.
                                                                                                                                                    LENGTH:
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Similarity 49.0%;
49; Conservative
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5. 5863798
                                                                                                   LE TYPE: protein
451 AA; 49762 MW; 1024670 CN;
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19406-5090
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                                                                                                                                                    451 amino acids
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                                                             47.78;
49.08;
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                                                Score 361; DB 2;
Pred. No. 8.84e-27;
17; Mismatches 34
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Pred. No. 8.84e-27;
17; Mismatches 34;
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                                                                                                                                                                                               Local Similarity
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wolffe, Susan A
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ADDRESSEE: Banner & Witcoff,
STREET: 1001 G Street, N.W.
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                     GSIVLDDVACTGHEAYLWSCSHRGWLSHNCGHHEDAGVIC 391
                                                                                                                                        VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
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Pred. No. 1.21e-25;
17; Mismatches 33
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                                            Sequence 6, Application US/08794795
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Sequence 6, Application US/08794795 Patent No. 5916766 GENERAL INFORMATION:
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                                                                                                                                                                                                                          399 VRIV-GSSNR-GRAEVYYSGTWGTICDDEWQNSDAIVFCRMLGY---SKGRAL-YKVGAG 452
                                                                                                                                                                                                                                                        Local Similarity
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
ENCE 495 AA; 49764 MW; 1218428 CN;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: ATTELECOMMUNICATION INFORMATION: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: ATG50009P FILING DATE: 22-MAY-1996 ATTORNEY/AGENT INFORMATION:
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CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Han, William T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-FEB-1997
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Pred. No. 3.61e-23;
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                                                                                                   Sequence 2, Application US/08200900A
                                                      Patent No. 5665566
GENERAL INFORMATION:
                                                                   Sequence 2, Application US/08200900A
Patent No. 5665566
                                                                                                                                                                                                                506 KGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546
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Local Similarity 48.5%;
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APPLICANT:
TITLE OF INVENTION: CL
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: ATG50009P
FILING DATE: 22-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
JENCE 520 AA; 52658 MW; 1340662 CN;
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REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
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LENGTH: 520 amino acid
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TOPOLOGY: linear
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SOFTWARE: FastSEQ for Windows Version
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Lysko, Paul
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Genetics Institute,
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Pred. No. 3.61e-23;
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CC CITY: Cambridge
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CC COMPUTER REDABLE FORM:
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Release 3.1A John F. Collins, Biocomputing Research Copyright (c) 1993-1998 University of Edinburgh, U. Distribution rights by Oxford Molecular Ltd Unit.

cn_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tabular output not generated. Mon Mar 13 10:34:56 2000; MasPar time 6.76 Seconds 353.990 Million cell updates/sec

Description: Perfect Score: Title: >US-09-147-947-6 (447-547) from US09147947A.pep (6 of 6) 757

Searched: 188963 segs, 23686106 residues

Scoring table: Sequence:

PAM 150 Gap 11

1 VRLMDGENKKEGRVEVFING.....KQDIGRHNCRHSEDAGVICD 101

Post-processing: Minimum Match Listing first 0% 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 28.103; Variance 102.859; scale 0.273

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

1		Olbert *			SUMMARIES		
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ω	9		585	Н	135		. 08
9	9		585	μ,	21	ce of a 90K	. 08
10	376	49.7	453	М	R05509	r receptor	5.02e-
11	7		453	ш	R27036	. scavang	. 02
12	σ	•	489	1	W39749	narcos	
13	g	•	518	_	(4)	phage rec	. 00
14	σ	•	451	ш	W19708		. 45
15	Ò		1785	۲	W64591		. 45
16	Φ	٠	451	Н	R27035		31
17	Q	•	451	٢	W08077	S.	·
18	9	•	451	_	R40802	to	.31
19	g		451	Н	R21512		. 98
20	(Ji		666	μ	W64590		. 07
21	S	σ,	1290	Н	W07609	on Ebner's gla	. 80
22	4		574	_	R40784		. 05
23	4	45.7	574	1-1	W81362	tokine regula	.05e-

RESULT
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w83361 standard; Protein; w83361; 17-FEB-1999 (first entry)

875

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Human neurotrypsin.

Human; neurotrypsin; tumour inhibition; neurological disease;

Human; neurotrypsin; tumour inhibition; neurological disease;

lung disease; gene therapy; drug development; stroke; brain injury;

neurodegeneration; neuroinflammatory disease; multiple sclerosis;

epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;

Lit Mole is account 1167 1162 1162 198 6 W54350 W23995 R54073 W87632 W35258 W17700 W06829 P70137 R59841 W81365 W46917 W39747 W39748 Y04374 R57283 Y13369 W35849 BOR CAMP-dependent Bacillus thuringiensis CryET4 protein sequenc Bacillus Amino acid sequence Human Human marcosk protein Human marcosk protein Human macrophage recep Amino acid sequence of Human scavenger recept Human liver cell clone Human Bovine enterokinase. CB5 prohormone conve

ALIGNMENTS

Sequence of a region of ApoE4L protease.
Human ApoE4L.
Human ApoE4Lx2.

Major neutralising

ant

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thuringiensis

protein

3.67e-25 3.67e-25 3.67e-25 3.67e-25 3.68e-24 1.68e-24 1.68e-24 1.68e-20 1.14e-00 1.06e+00 1.06e+00 1.06e+00 1.02e+01 1.92e+01 1.92e+01 1.92e+01 3.45e+01 3.4

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ApoE4Lx2 protease

Db	A A A B B	A C C C C C C C C C C C C C C C C C C C
507 GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVICD 547	Query Match 100.0%; Score 757; DB 1; Length 822; Best Local Similarity 100.0%; Pred. No. 3.21e-73; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 447 VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506	RESULT 1 ID W99087 standard; Protein; 822 AA. RAC W99087, DT 13-MAY-1999 (first entry) DE Human serine protease BSSP-3. RW Serine protease; BSSP-3; brain tissue. Serine protease; BSSP-3; brain tissue. RW Serine protease; BSSP-3; brain tissue. RW Serine protease; BSSP-3; brain tissue. PN W09905290-A1. PD 04-FEB-1999. P1 SUNTORY LTD. P2 24-JUL-1997; JP-213969. RA-JUL-1997; JP-213969. RA-JUL-1997; JP-213969. PA (SUNR) SUNFORY LTD. PR (SUNR) SUNFORY LTD. PR (SUNR) SUNFORY LTD. PR N-PSDB; X19024. PR N-PSDB;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents human neurotrypsin. Neurotrypsin proteins CC and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or retina; (ii) to minimise tissue damage CC metastases, e.g. of brain or retina; (ii) to minimise tissue damage CC caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration, neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) to increase survival of damaged neurons (e.g. in cases of hypoxia, ischaemia, nerve transection) and to stimulate regeneration and/or restoration of synapses; (v) to treat or prevent retinal disorders (e.g. degeneration or neoangiogenesis); (vi) to prevent approxis (or other CC degeneration or neoangiogenesis); (vi) to prevent approxis (or other causes of cell death) in the nervous system; (vii) to regenerate brain CC and/or nervous tissue; (viii) to treat pain; (ix) to improve brain. CC performance, including learning and memory; (x) to treat or prevent approximate of psychiatric disorders; and (xi) to treat brain or lung conjury associated with protease expression (specifically emphysema or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                   W09849322-A1.
05-NOV-1998.
05-NOV-1998; IB0625.
24-APR-1997; CH-000966.
26-APR-1997; CH-000966.
tumours, treatment of neurological or lung disease, including by gene therapy and in drug development Claim 1; Page 29-32; 50pp; English.

The present sequence represents mouse neurotrypsin. Neurotrypsin p and polynucleotides can be used: (i) to inhibit tumours, including metastases, e.g. of brain or retina; (ii) to minimise tissue damage caused by stroke or brain injury (having a protective effect on the penumbra zone); (iii) to treat or prevent neurodegeneration,
                                                                                                                                                                                               N-PSDB; V72590.
                                                                                                                                                                                                                                      Sonderegger P;
                                                                                                                                                                                                                                                                                                                                                                                     emphysema; bronchitis.
                                                                                                                                                                                                                                                                                                                                                                                                    ung disease; gene therapy; drug development; stroke; brain injur eurodegeneration; neuroinflammatory disease; multiple sclerosis; epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; neurotrypsin; tumour inhibition; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse neurotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W83362 standard; Protein; 761
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tumours, treatment of neurological or lung
gene therapy and in drug development
Claim 1; Page 20-24; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V72589.
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W09849322-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1997; CH-000966.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      507 GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVICD
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Local Similarity 100.0%;
hes 101; Conservative
                                                                                                                                                                                                                                                                                                                                                               musculus.
                                                                                                                                                                       human and murine neurotrypsin - used, e.g.
                                                                                                                                                                                                                99-009438/01.
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Pred. No. 3.21e-73;
0; Mismatches of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used, e.g. for
or lung disease,
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                          damage
on the
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Best Local s
Matches 9
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Best Local :
12-APR-1999 (first entry)
Human cytokine regulatory factor CYTRF.
Cytokine regulatory factor; cyclophilin C-associated protein;
CYTRF; CYCAP; antiinflammatory; inflammation; autoimmune disease;
multiple sclerosis; rheumatoid arthritis; ankylosing spondylitis;
meningitis; herpes encephalitis; viral meningoencephalitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroinflammatory disease (e.g. multiple sclerosis) or epilepsy; (iv) t increase survival of damaged neurons (e.g. in cases of hypoxia, ischaemia, nerve transection) and to stimulate regeneration and/or restoration of synapses; (v) to treat or prevent retinal disorders (e.g. degeneration or neoangiogenesis); (vi) to prevent apoptosis (or other causes of cell death) in the nervous system; (vii) to regenerate brain and/or nervous tissue; (viii) to treat pain; (ix) to improve brain performance, including learning and memory; (x) to treat or prevent a wide range of psychiatric disorders; and (xi) to treat brain or lung
                                                                                                                                           W81363 standard; Protein; W81363; 12-APR-1999 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-1999.
24-JUL-1998; J03324.
24-JUL-1997; JP-213969.
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761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUNR) SUNTORY LTD.
Tsuruoka N, Yamaguchi N, Yamashiro
WPI; 99-142942/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
W09905290-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for potential serine protease
Example 1; Page 51-54; 69pp; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New serine protease expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; X19027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 95.6%;
Similarity 92.1%;
93; Conservative
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93; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         761 AA;
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BSSP-3; brain tissue.
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92.1%;
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Pred. No. 1
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No. 1.97e-69;
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1.97e-69;
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    used in screening

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CYTRF), also known as cyclophilin C-associated protein (CYCAP).

Methods are provided for the modulation of cytokine production by T C helper cells using CYTRF (especially human CYTRF). A pharmaceutical composition comprising CYTRF as an active agent is administered in CYTRF or in vivo, and can act on mature, committed Th1 type T cells to decrease the production of pro-inflammatory cytokines, or to skew the commitment of precursor T helper cells to Th1 or a Th1 cytokine CYTRF is useful in the diagnosis and CYTRF treatment of autoimmune diseases (e.g. multiple sclerosis, CYTRF and degenerative joint diseases including and treatment of autoimmune diseases (e.g. multiple sclerosis, CYTRF and degenerative joint diseases including CYTRF and degenerative point diseases including CYTRF and degenerative arthritis), and inflammation CYTRF infection (e.g. meningitis, CYTRF encephalitis, viral meningencephalitis and viral hepatitis), CYTRF infection (e.g. meningitis, CYTRF encephalitis, CYTRF and measles) and skin sensitivity (e.g. graft crejection and graft vs host disease). CYTRF signalling and related
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Best Loc
Matches
W09308215-A.
29-APR-1993.
15-OCT-1992; U08878.
16-OCT-1991; US-777111.
R 15-OCT-1992; US-961404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathways are also useful for modelling and screening new pharmacological agents. The administration of agents that block CYTRF action (e.g antibodies) are useful in reducing unwanted allergic responses, especially in asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reduction of pro-inflammatory cytokines in a T cell population - useful in the diagnosis using cytokine regulatory factor (CYTRF), useful in the diagnosis and treatment of pro-inflammatory conditions

Disclosure; Page 47-51; 77pp; English.

This is the amino acid sequence of human cytokine regulatory factor
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gp85-97 clone 18 prod.
Glycoprotein; lectin; Mac-2;
                                                                                                                                                                                                                                                                                                                                                                                          phytoheamagglutinin; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R36533 standard;
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                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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13-JUN-1997;
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Similarity 52.0%;
52; Conservative
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US-049578.
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diagnosis; therapy; human.
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Pred.
17; M
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No. 1.08e-31;
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Claim 1, Page 41; 57pp; English.

CC SK-BR-3 gp97 recovered in partially proteolysed form was denatured common the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the stands of clone 218 were sequence that encodes a novel of state of the state of the stands of clone 218 were sequence with pHA activation of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of 
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17-FEB-1993;
17-FEB-1992;
Immunoregulin-95 is a 90K tumour-associated antigen purified from the culture fluid of the human breast cancer cell line, CG-5, the serum of a breast cancer patient, or the ascitic fluid mol. wt. ovarian cancer patient. The native antigen, which has a mol. wt. of bkD, is present as a high mol. wt. complex. Homology in the region has 35-80 of the 90K antigen is found with type I macrophage
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New glyco:protein complex binding to human lectin interferes with PHA activation of lymphocytes for infectious diseases, etc.
                                                                                                                                                                                                                                     Recombinant DNA - encoding immuno-regulin-95
                                                                                                                                                                                                                                                                                                                                       Azam M, Iacobelli
WPI; 93-272884/34.
                                                                                                                                                                                                                                                                                                                                                     17-FEB-1992; IT-RM0100.
(PLAC ) MAX PLANCK GES FOERDERUNG (UYCH-) UNIV CHIETI ANNUNIO G D. Azam M, Iacobelli S, Natoli C, WPI: 93-77984/24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-1994
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breast cance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
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93-152424/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= glycosylation site
/note= "see also AAs 125,192,362,398,551,580"
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Pred. No. 1.08e-31;
17; Mismatches 31
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Query Match
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                                     90K Tumour-associated antigen - purified from serum of breast cancer patient or ascitic fluid from ovarian cancer patient Claim 1; Figure 1; 73pp; English.

The purified 90K antigen or its antigenic determinant containin fragment can be assayed to diagnose a disorder, such as cancer especially breast or ovarian cancer) or a viral infection, inflammation, autoimmune disease and/or arthritis in a patient. It may also be used in the preperation of an agent for the treatment of these disorders.
                                                                                                                                                                                                                            02-SEP-1993; I
16-FEB-1993; I
17-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scavenger receptor; sea urchin speract receptor; and human lymphocyte glycoprotein Tl/Leu-1.
Sequence 585 AA;
                                                                                                                                                                                       17-FEB-1992; IT-RM0099.
(UYCH-) UNIV CHIETI ANNUNZIO G D.
(UYNY ) UNIV NEW YORK STATE.
Iacobelli S, Natoli C, Schlessinger
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les 52; Conse
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Larity 52.0%;
Conservative
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lated 90K antigen.
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   391; DB 1;
No. 1.08e-31;
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No. 1.08e-31;
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                                                                                                                                                                                                                                                               PT diagnosis and therapy of cancer, HIV and auto-immune diseases
PS Claim 2; pages 45-48; 68pp; English.
CC 90K antigen has an apparent molecular weight of approx. 95 kd. It is
CC with cancer and also in patients with HIV. It reacts with MAb SP-2
CC which was prod. by immunising mice with proteins that had been
CC released into tissue culture fluid by human MCF-7 breast cancer
CC cells. MAb SP-2 cell line is deposited at the institut Pasteur,
CC Paris, Accession number 1-1083. 90K is also present in normal
CC subjects. It is purified from the culture fluid of the human breast
CC cancer cell line; CG-5. N-terminal sequencing of the 90K antigen
CC was used to design a 'guessmer' nucleotide sequence (Q48171) as a
CC probe to screen a lambda-gtl0 library prepd. from MCF 70ly4+ RNA.
CC The complete nucleotide sequence of isolated clones is given in
CC Gental Control of the sequence of solated clones is given in
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Matches
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R05509;
R05509;
23-OCT-1990
Scavenger rec
                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of a 90K tumour-associated antigen, of binding to SP-2 (Accession No. I-1083).
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03-FEB-1994
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R40213 standard;
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WPI; 93-272885/34.
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/note= "see also AAs 125,192,363,398,551,580"
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                                       protein;
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Pred. No. 1.08e-31;
17; Mismatches 31
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WO9005748-A Acylated lipoprotein

low

density lipoprotein; aLDL; atherosclerotic plaque

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            N-PDSB; 028540.

Treatment and diagnosis of endotoxaemia and related disease states - using a polypeptide fragment of the extracellular portion of a macrophage scavenger receptor protein Disclosure; Page 38; 56pp; English.

The bovine scavanger receptor protein sequence was deduced from DNA sequence obtd. by screening a bovine lung cDNA library with degenerate probes designed based on fragments of the purified scavanger receptor protein. The scavanger receptor protein has binding capacity for acetylated low density lipoprotein (LDL) and binding capacity for acetylated low density lipoprotein (LDL) and the scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein scavanger receptor protein sc
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has affinity for acetylated low density lipoprotein and
corresponding antibodies and DNA sequences.

Disclosure; 79pp; English.

Receptor protein, and fragments and analogues thereof may be
imobilised on a support and used in assay and purification of the
aldL target. Labelled Abs, raised to the protein may be injected
into the vascular system to detect the presence of atherosclerot:
                                                                                                                                                                                                                                                                                                                                03-SEP-1992.
21-FEB-1992; U01370.
22-FEB-1991; US-662227
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R27036 standard;
R27036;
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15-NOV-1988; US-272002.
(MASI) Massachusetts In
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N-PSDB; Q04926.
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272. .:
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Pred. No. 5.02e-30;
17; Mismatches 34
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19-MAY-1997; US-794795.
04-FEB-1997; US-794795.
23-MAY-1996; US-017699.
(SMIK ) SMITHKLINE BEECHAM CORP.
Adamou JE, Elshourbagy NAE, Gross
WPI; 98-001786/01.
                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a mouse Macro scavenger receptor (MMacroSR) which is used to confirm the presence of a novel human macro scavenger receptor (HMacroSR). This polypeptide and resulting antibodies can be used to treat cardiovascular diseases, including atherosclerosis, hypertension myocardial and cerebral infarction, angina, organ failure, stroke, gangrene, and loss of function in the extremities. They can also be used to treat or diagnose various macrophage and other immune cell related host defense disorders, septic shock, pancreatitis, multiple organ failure, endotoxaemia and infections caused by gram negative and content in the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the conte
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W39749;
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                                                                                                                                                                                                                                   gram positive bacteria. Agonists and antagonists may also be used to treat these diseases. The polynucleotide can be used to detect mutated forms of HMarcoSR which may be associated with a dysfunction and can define a diagnosis of a disease (or susceptibility to a disease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marco scavenger receptor; MarcoSR; mouse; antibodies; treatment; diagnosis; cardiovascular disease; macrophage; bacterial infection; immune cell related host cell disorder; pancreatitis; organ fallure; endotoxaemia; agonist; antagonist; dysfunction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections etc.
Disclosure; Fig 1; 45pp;
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26-NOV-1997.
                                                                                                                                                            Sequence
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        Similarity
54; Conser
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Score 369; DB 1; Pred. No. 3.00e-29; 17; Mismatches 24
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Pred. No. 5.02e-30;
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        24;
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                                                                              Length 489
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    Indels
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        <u>ن</u>
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Gaps
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507 GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546

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δõ
                                                                                                                                                         and related DNA, anti-sense probes and antibodies, involved in PT immune defence and phagocytosis
PS Claim 10; Fig 2A-B; 62pp; English.
A novel macrophage receptor with a collagenous domain, named MARCO (w03561), is a membrane-bound trimeric protein which is expressed strongly after birth in a subset of macrophages in mouse spleen and lymph nodes. It binds to bacteria but not to yeast, and probably C plays a role in immune defence and/or phagocytosis. The amino acid Sequence of MARCO was deduced from DNA (see also T39340) obtd. from C a mouse macrophage cDNA library. Recombinant MARCO can be produced in transformed host cells. It is used to raise antibodies useful in detecting MARCO or interfering with its function.
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Best Local
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22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W03561 standard;
                                                                                                                                                                                                                                                                                                                                                                                          Elomaa O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-1996.
19-FEB-1996; FI0091.
21-FEB-1995; US-392367.
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                                                      447
                                                                                                                                                                                                                                                                                                                                                                                                                     (ELOM/) ELOMAA O.
(KANG/) KANGAS M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO9626219-A1.
                                                                                   423
                                                                                                                                                                                                                                                                                                                                                                                                       TRYG/) TRYGGVASON K.
507 GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546
                                                                                                                        Local
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                 GNIWLDNVNCRGTENSLWDCSKNSWGNHNCVHNEDAGVEC 517
                                                                                                                                                                                                                                                                                                                                                                             96-402322/40.
                                                     VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                                             VRIMGGTNR---GRAEVYYNNEWGTICDDDWDNNDATVFCRMLGY----SRGRALSSYGGGS 477
                                                                                                             Similarity
54; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor with collagenous domain (MARCO) receptor-collagenous; MARCO; immune defe
                                                                                                          48.7%;
larity 54.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "collagenous structure characterised by Gly-X-X repeats with one interruption (Ala-Glu-Lys at 174-176)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "hydrophilic 87. .89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "putative N-glycosylation
138. .140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "hydrophilic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Glycosylation
/note= "putative glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Domain-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein; 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                       Tryggvason
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "globular C-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain-IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain-III
                                                                                                          Score 369; DB 1; Le
Pred. No. 3.00e-29;
17; Mismatches 24;
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                                                                                                                                    Length 518;
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RESULT RESULT WAY AC WAY AC WAY AC WAY AC SOLUTION OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCORDANCE OF ACCO
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Best Local
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                                                                                                             Homo sapiens.

WO9830697-A2.

16-JUL-1998.

09-JAN-1998; D00096.

18-JUL-1997; DE-030997.

09-JAN-1997; DE-000519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibit complement activation, cytokine release or nitric oxide production induced by LTA released by the Gram-positive bacteria. In addition to treating Gram-positive septic shock, the MSRP can be used to screen for other compounds for treating Gram-positive septic shock. MSRP can also be used to purify, label or detect LTA or LTA-containing cells. MSRP, active MSRP fragments, anti-MSRP antibodies or other compounds that inhibit binding of Gram-positive bacteria to MSRP can be used to treat pathologies such as septicamnia, Gram-positive bacterial infection, Gram-positive septicaemia or Gram-positive or Gram-negative septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the human macrophage scavenger receptor protein (MSRP). MSRP binds specifically to the lipoteichoic acid (LTA) residues on the Gram-positive bacterial cell wall. MSRP exhibit unusually broad binding specificity for polyanionic ligands, and have been implicated in atherosclerosis and a variety of host defence functions. This protein can be used in the method of the invention is for the treatment of septicaemia caused by Gram-positive bacteria. The method comprises administration of a MSRP in an amount sufficient to
                                                                                                                                                                                                                                                                                                                        Human SRCR protein.
Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment; nervous system; medullo-blastoma; glioma; breast; detection;
                            Mollenhauer J, Poustka WPI; 98-399136/34.
                                                                                                                                                                                                                                                                                                     autoantibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           W64591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W64591 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gram-positive septicaemia Sequence 451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               administration of macrophage scavenger r
Disclosure; Column 23-26; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joiner KA, Krieger WPI; 97-258236/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macrophage scavenger receptor protein.
Macrophage scavenger receptor protein; MSRP; human;
LTA; Gram-positive bacteria; cell wall; atherosclerc
septicaemia; inhibitor; complement activation; cytol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W19708;
19-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W19708 standard; Protein; 451
                                                                                       (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-1998 (first entry)
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17-NOV-1993; US-154365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447
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Similarity 49.0%;
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Pred.
17; M
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1. No. 6.45e-29;
1. no. f.45e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor protein
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ch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:34:27 2000; MasPar time 10.39 Seconds 458.750 Million cell updates/sec

Title:

Description: Perfect Score: >US-09-147-947-6 (447-547) from US09147947A.pep (6 of 6) 757

1 VRLMDGENKKEGRVEVFING.....KQDIGRHNCRHSEDAGVICD 101

Scoring table: PAM 150 Gap 11 Sequence:

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir62 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 37.980; Variance 62.138; scale 0.611

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	% Query Match	Length	DB	SUMMARIES	Description	Pred. No.
سو ر	724		761	งง	JC5759	ific ser	2.66e-1
∞	391	51.7	585	N 1	114893 A47161	scavenger receptor cy Mac-2-binding glycopr	4.71e-86 7.87e-68
۵(385	0	453	N	S08276		.19e-6
₅	381	0	454	N	I46862	()	.00e-6
თ	380	0	1116	2	S36077		.48e-6
7	380	0	1149	N	138006		.48e-6
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, ₁ .	3 G	48.7	518	N	A55840		1.51e-62
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۰ (J.	362	4 /	1436	N	A46496	antigen WC1.1 precurs	.15e-6
4 r	1 to 1	•	4 1) K	A38415	macrophage scavenger	.24e-6
1 L	357	47.2	5/7	N	A53202	C-assoc	1.12e-5
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17	351	0	532	N	A32751	eceptor pi	3.01e-5
18	350	6	1290	ν	A57190	rsor	.20e-5
19	345	ŗ	600	Ν	S56744	mucin (clone pGM7-1)	.04e-5
20	343	45.3	504	N	S56745	mucin (clone pGM31-1)	.40e-5
21	323	2	468	N	S26741		.30e-5
22	320	42.3	626	N	149100	mscd6 precursor - mou	.60e-5
23	157	20.7	1034	بـــ	A53663	enteropeptidase (EC 3	.90e-1

ALIGNMENTS

GPIHMDNVKCTGNEKALADCVKODIGRHNCRHSEDAGVICD 486	Db 446 GP
IRLYDGENKKEGRVEVFVNGQWGTICDDGWTDKHAAVICRQLGYKGPARARTMAYFGEGK 445 : : : :	Db 386 IR : Qy 447 VR
Query Match 95.6%; Score 724; DB 2; Length 761; Best Local Similarity 92.1%; Pred. No. 2.66e-150; Matches 93; Conservative 7; Mismatches 1; Indels 0; Gaps 0;	Query Matc Best Local Matches
#active_sit #active_sit #length 761 #ma	562,612,711 SUMMARY
# # # hr O. O.	513-516 517-755 93,521,569
/3-3/2, #domain scavenger receptor cysteine-rich #status predicted #label SRC\	166-266, 2/3-3/2, 386-486
<pre>#domain kringle-like #status predicted #label KRI\ #domain scavenger receptor cysteine-rich domain homology #label SRC7\</pre>	85-157 163-266
glycoprotein; hydrolase; serine proteinase	KEYWORDS
##experimental_source brain FICATION #superfamily trypsin homology; scavenger receptor Cystrino-rich domain homology	##experi
#residues 1-761 ##label YAM #cross-references DDBJ:D89871	##residues
##molecule type mrna	#accession
#cross-references MUID:98008848	#cross-re
with a kringle-like structure and three scavenger receptor	# C+ C+
(1997) 239:386-392	#journal
Yamamura, Y.; Yamashiro, K.; Tsuruoka, N.; Nakazato, H.; Tsuiiimura, A.: Yamagurchi, N	#authors
	REFERENCE
24-Jan-1996 #sequence_revision is-mar-1996 #text_change	DAIE
#formal_name Mus musculus #common_name house mouse	ORGANISM
brain-specific serine proteinase (EC 3.4.21) - mouse	TITLE
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 ##residues
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                                                                                                                                    Ullrich, A.; Sures, I.; D'Egidio, M.; Jallal, B.; Po
T.J.; Herbst, R.; Dreps, A.; Azam, M.; Rubinstein,
Natoli, C.; Shawyer, L.K.; Schlessinger, J.; Iacob
                                                                                                  T.J.; Herbst, R.; Dreps, A.; Azam, M.; Ru
Natoli, C.; Shawver, L.K.; Schlessinger,
J. Biol. Chem. (1994) 269:18401-18407
The secreted tumor-associated antigen 90K
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#length
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Cloning and characterization of a human Mac-2-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                          A47161 #type complete
Mac-2-binding glycoprotein precursor - human
90K tumor_associated protein precursor
#formal_name Homo sapiens #common_name man
05-May-1995 #sequence_revision 05-May-1995 #text_change
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Origins of immunity: transcription
effector genes of the vertebrate
sea urchin coelomocytes.
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urchin (Strongylocentrotus purpuratus)
#formal_name Strongylocentrotus purpuratus #common_name
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:es EMBL:AF064259; NID:g4165052; PID:g4165053;
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                                                                                                                                                          macrophage scavenger receptor type I #formal_name Bos primigenius taurus #common_name cattle 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
Matsudaira, P.; Krieger, M.
Nature (1990) 343:531-535
Type I macrophage scavenger receptor and collagen-like coiled coils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenberg, I.; Cherayil, B.J.; Isselbacher, K.J.; Pi
J. Biol. Chem. (1991) 266:18731-18736
Mac-2-binding glycoproteins. Putative ligands for a
beta-galactoside lectin.
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Purification and characterization of a 90 kDa pro
                                                             Kodama, T.; Freeman, M.; Rohrer,
Matsudaira, P.; Krieger, M.
                                                                                                                            S0827
                                                                                                                                                                                                                        LDL receptor I, macrophage - bovine
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the reported molecular weight of this protein,
designated Mac-2-binding glycoprotein 2 (MZBP-2)
70K; the amino-terminal sequence of a related fr
98K, designated MZBP-1, could not be determined
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                                                                                                                                                                                                                                                                                          350-453
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#accession I46862
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9-452
507
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PID:g735
##note part of this sequence was confirmed by protein
                                          413
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  GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546
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                                        GPIWLNEVPCLGMESSIEECKIRQWGVRVCSHGEDAGVTC 452
                                                                                 VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
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Similarity 49.0%;
49; Conservative
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cysteine-rich domain homology
alternative splicing; coiled coil; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bickel, P.E.; Freeman, M.W.
J. Clin. Invest. (1992) 90:1450-1457
Rabbit aortic smooth muscle cells express inducible
macrophage scavenger receptor messenger RNA that is
from endothelial cells.
                                                                                                                                                                                                                                                  #length
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#formal_name Oryctolagus cuniculus #common_name domestic
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Pred. No. 2.19e-66;
17; Mismatches 33
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Pred. No. 2.00e-65;
20; Mismatches 31;
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                                                #authors Law, S.K.; Micklem, K.J.; Shaw, J.M.; Zha Willis, A.C.; Mason, D.Y.
#journal Eur. J. Immunol. (1993) 23:230-2325
#title A new macrophage differentiation antigen the scavenger receptor superfamily.
#cross-references_MUID:93380506
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##status preliminary;
##molecule_type mRNA
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##cross-references EMBL:Z22968; NID:g312141; PID:g312142
#TICATION #superfamily scavenger receptor cysteine-rich
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Local Similarity 51.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                     M130 antigen (extracellular variant) - human #formal_name Homo sapiens #common_name man 17-May-1996 #sequence_revision 17-May-1996 #text_change 02-Aug-1996  
138006; S35768
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A new macrophage differentiation antigen which
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Pred. No. 3.48e-65;
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##cross-references EMBL:222971; NID:g312147; PID:g312148
CLASSIFICATION #superfamily scavenger receptor cysteine-rich
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Best Local Similarity 51.0%;
Matches 51; Conservative
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cession I38004
##status preliminary;
##molecule_type mRNA
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##cross-references EMBL:Z22969; NID:g312143; PID:g312144
##cross-references EMBL:Z22969; NID:g312143; PID:g312144
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M130 antigen (cytosolic variant 1) - human
#formal_name Homo sapiens #common_name man
17-May-1996 #sequence_revision 17-May-1996
07-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                      Willis, A.C.; Mason, D.Y.
Eur. J. Immunol. (1993) 23:2320-2325
A new macrophage differentiation antigen which is the scavenger receptor superfamily.
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#domain scavenger receptor cysteine-rich domain
#label SRC9
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#label SRC4\
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#label SRC6\
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Db 774 GPIWLDEMKCNGKESRIWQCHSHGWGQQNCRHKEDAGVIC 813 : : : : : : : : : : : :	Qy Qy
Db 714 LRLVNGGGRCAGRVEIYHEGSWGTICDDSWDLSDAHVVCRQLGGGEAINATGSAHFGEGT 773 : :: : :	Qy dd
Query Match 50.2%; Score 380; DB 2; Length 1156; Best Local Similarity 51.0%; Pred. No. 3.48e-65; Matches 51; Conservative 19; Mismatches 30; Indels 0; Gaps 0;	
SUMMARY #length 1156 #molecular-weight 125352 #checksum 9043	SU
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#fature SNOV 365-468 #domain homology #domain sport receptor cysteine-rich domain homology	
43-147 #domain scavenger receptor cysteine-rich domain homology	
##105085 references EMBL: 222970; NID: g312145; PID: g312146 CLASSIFICATION #superfamily scavenger receptor cysteine-rich domain homology KEYWORDS cytosol FEATURE	H K C
<pre>preliminary; tran le_type mRNA</pre>	
ss-references MUID:93380506	
#journal Eur. J. Immunol. (1993) 23:2320-2325 #title A new macrophage differentiation antigen which is a member of the scavenger receptor superfamily.	
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ACCESSIONS 138005; S36079 REFERENCE 138003	2 A
RESULT 9 I38005 #type complete TITLE M130 antigen (cytosolic variant 2) - human ORGANISM #formal_name Homo sapiens #common_name man 17-May-1996 #sequence_revision 17-May-1996 #text_change	D T I
OF 774 GPLWIDEMKCNGKESKIW/CHSHGWQNCHKEEDGVIC 813	<u>ي</u> و
14 LENDWOGERCHOKKEINEGSWOTTCDDWDLSCHAPVCKQ 	9 5
Query Match 50.2%; Score 380; DB 2; Length 1151; Best Local Similarity 51.0%; Pred. No. 3.48e-65; Matches 51; Conservative 19; Mismatches 30; Indels 0; Gaps	!
lar-weight 124820 #checksum 1481	JS
#label SRC8\ 1-1024 #domain scavenger receptor cysteine-rich domain	
816-920 #domain scavenger receptor cysteine-rich domain homology	

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Best Local Similarity 48.0%;
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#title
                                                  418-518
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#cross-references MUID:95171455
#accession A55840
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                                                                                                    ###CFOSTON #superfamily scavenger receptor cysteine-rich domain
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##molecule_type nucleic acid
##residues 1-454 ##label DOI
                                                                                                                                                                                ##molecule_type mRNA
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#superfamily unassigned collagens; scavenger receptor
cysteine-rich domain homology
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                                                                                                                                                                                                                                                                                                                                   Tryggvason, K.
Cell (1995) 80:603-609
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macrophage bacteria-binding receptor MARCO - mouse
#formal_name Mus musculus #common_name house mouse
23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change
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Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger
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Sormunen, R.; Liakka,
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    #length 518
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A.; Thesleff,
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I.; Kraal,
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Query Match 48.6%;
Best Local Similarity 49.0%;
Matches 49; Conservative
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Best Local
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Copeland, N.G.; Jenkins, N.A.; Krieger, M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8810-8814
An ancient, highly conserved family of cysteine-rich produced by cloning type I and type II murine macrophage scavenger receptors.
#cross-references MUID:91062370
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#title
                                                                                                                                                                                                                                                                                                                                                                        M.W.; Krieger, M.
J. Lipid Res. (1993) 34:983-1000
#title Structures and high and low affinity ligand binding properties of murine type I and type II macrophage scavenger receptors.
#cross-references_MUID:93359822
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#accession B44407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status preliminary
##molecule_type mRNA
##residues 349-458 ##label FRE
##cross-references GB:M59445; GB:M3
##CTOSS-references GB:M59445; GB:M3
                                                                                                                                                                                                  ##residues - 1. 5-458 ##label RES
##cross-references GB:L04274; NID:g293745; PIDN:AAA39747.1; PID:g293746
##CTOSS-references GB:L04274; NID:g293745; Scavenger receptor cysteine-rich domain homology
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##molecule_type nucleic acid
##residues 1-458 ##label DOI
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##note sequence extracted from NCBI backbone (NCBIP:123207)
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Similarity 54.08;
54; Conservation
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Charged collagen structure mediates the recognition of negatively charged macromolecules by macrophage scavenger
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                       Score 368; DB 2;
Pred. No. 2.63e-62;
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#accession A46496
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##experimental_source CD4-CD8- gamma delta T lymphocytes
##note sequence extracted from NCBI backbone (NCBIP:117475)
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Members of the novel WCl gene family are differentially expressed on subsets of bovine CD4-CD8- gamma delta T
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antigen WC1.1 precursor - bovine
#formal_name Bos primigenius taurus #common_name cattle
18-Jun-1993 #sequence_revision 19-May-1994 #text_change
13-Nov-1998
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J. Immunol. (1992) 149:3273-3277

Molecular characterization of the WCl antigen expressed specifically on bovine CD4-CD8- gamma deita T lymphocytes
    #length 1436
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                   #domain scavenger receptor cysteine-rich domain homology
#label SR11
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#molecular-weight 154196
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Best Local Similarity 49.0%;
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Best Local
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#authors Emi, M.; Asaoka, H.; Matsumoto, A.; Itakura, H.; Kurihara,
Y.; Wada, Y.; Kanamori, H.; Yazaki, Y.; Takahashi, E.;
Lepert, M.; Lalouel, J.; Kodama, T.; Mukai, T.

#journal J. Biol. Chem. (1993) 268:2120-2125
#title Structure, organization, and chromosomal mapping of the human
#title macrophage scavenger receptor gene.
#cross-references MUID:93131971
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#accession A38415
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##molecule_type nucleic acid
##residues 155-272 ##label EMI
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##cross-references GB:D90187; NID:g219989; P
PID:d1014913; PID:g219990
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##residues
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.p_position 8p22-8p22
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Local Similarity 53.0%;
hes 53; Conservation
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                                                                                          VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
    GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.; Hayakawa, I.; Kanamori, H.; Aburatani, H.; Takaku, F. Suzuki, H.; Kobari, Y.; Miyai, T.; Takahashi, K.; Cohen, E.H.; Wydro, R.; Housman, D.E.; Kodama, T. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9133-9137
Human macrophage scavenger receptors: primary structure, expression, and localization in atherosclerotic lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily unassigned collagens; scavenger receptor
                                                                                                                                                                                                                                                                                                                                                                                  alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A44408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsumoto, A.; Naito, M.; Itakura, H.; Ikemoto, S.; Asaoka, H.; Hayakawa, I.; Kanamori, H.; Aburatani, H.; Takaku, F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      macrophage scavenger receptor splice form I
#formal_name Homo sapiens #common_name man
                                                                                                                                                                                                                                                                                     #length 451 #molecular-weight 49762 #checksum
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                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          cysteine-rich domain homology
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                                                                                                                                                                                                                                                                                                                                 #domain scavenger receptor cysteine-rich domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence extracted from NCBI
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                                                                                                                                                                                     Score 361; DB 2;
Pred. No. 1.24e-60;
17; Mismatches 34
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Search completed: Mon Mar 13 10:34:39 2000 Job time : 12 secs.
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REFERENCE
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ENTRY
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#journal
#title
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Fauthors Friedman, J.; Trahey, M.; Weissman, I.
Foc. Natl. Acad. Sci. U.S.A. (1993) 90:6815-6819
Foc. Natl. Acad. Sci. U.S.A. (1993) 90:6815-6819
Cloning and characterization of cyclophilin C-associated
protein: a candidate natural cellular ligand for
cyclophilin C.
fcross-references MUID:93342080
#accession A48231
                                                                                                                                                                                                                                                                                              ery Match 47.2%;
st Local Similarity 50.0%;
tches 50; Conservative
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journal J. Biol. Chem. (1994) 269:5512-5517

title Cloning and expression of a mouse macrophage cDNA coding for a membrane glycoprotein of the scavenger receptor cysteine-rich domain family.

pross-references MUID:94164889

accession A53202
                                                                                                                                                                                            ##molecule_type mRNA 1-24,'G',26-227,'P',229-465,'NE',468-572,'LH' ##label'...
FRI
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1-577 ##label CHI
##restidues 1-577 ##label CHI
##ross-references EMBL:X67809; NID:9297032; PID:9297033; GB:X67803
##cross-references EMBL:X67809; NID:9297032; PID:9297033; GB:X67803
##note sequence appears consistent with either a GPI anchor or
transmembrane domain near the carboxyl end
                                                                                                  FC7 SPIHVDNVKCTGNERSLADCIKODIGRHNCRHSEDAGVIC 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##cross-references GB:L16894; NID:g397799; PID:g397800
                                                                                                                                   84 GPIMLDEVECTGTESSLASCRSLGWMVSRCGHEKDAGVVC 123
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Cyclophilin C-associated protein MAMA/CyCAP precursor -
MAC-2-binding glycoprotein homolog; murine adherent
macrophage (MAWA) protein

#formal_name Mus musculus #common_name house mouse
19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                 #domain signal sequence #status predicted #label SIG\
#domain scavenger receptor cysteine-rich domain homology
#label SRC
#length 577 #molecular-weight 64491 #checksum 6506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *superfamily scavenger receptor cysteine-rich domain homology cell surface component; glycoprotein; membrane protein
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A53202
                                                                                                                                                                                                                                                                                              Score 357; DB 2; Length 577; Pred. No. 1.12e-59; 16; Mismatches 34; Indels
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US-09-147-947-6-06.rspt At the sound

(MT)

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protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Mar 13 10:33:52 2000: MasPar time 16.67 Seconds 420.188 Million cell updates/sec

Description:
Perfect Score:
Sequence: Title: >US-09-147-947-6 (447-547) from US09147947A.pep (6 of 6) 757 1 VRLMDGENKKEGRVEVFING.....KQDIGRHNCRHSEDAGVICD 101

Scoring table: PAM 150 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb112
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 37.831; Variance 59.275; scale 0.638

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20 20 20 20 20 20 20 20	ง ง ง	Result No.
4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	466	Score
500.22 50	61.6	Query
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SNCK DOMAIN, MEMBRANE SP85. MAC-2 BINDING PROTEIN M130 ANTIGEN PECURSOR M130 ANTIGEN, CYTOPLAS M130 ANTIGEN, CYTOPLAS PANCREAS CANCER-ASSOCI MAMA. BACTERIA BINDING MACRO CRP-DUCTIN PRECURSOR (LYSYL OXIDASE-LIKE PRO LYSYL OXIDASE-RELATED DMBT1/6KB.1 PROTEIN PR DMBT1/FKB.1 PROTEIN PR DMST1/FKB.1 PROTEIN PR DMST1/FKB.1 PROTEIN UNKNOWN MRNA, PARTIAL LYSYL OXIDASE HOMOLOG LYSYL OXIDASE RELATED	SCAVENGER RECEPTOR CYS	Description
4.190e-74 4.190e-74 4.190e-71 4.499e-71 4.499e-68 4.499e-68 4.499e-68 4.55466-66 6.666 6.666 6.666 6.666 6.666 6.666 6.666 6.6666 6.6666 6.6666	7.20e-90 6.99e-76	Pred. No.

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	SCAVENGER-RECEPTOR PRO	T-CELL DIFFERENTIATION	SP-ALPHA.	SP-ALPHA.	CD6B.	CD6D.	CD6C.	•	RE		SP ALPHA.		LYSYL OXIDASE-RELATED	MEMBRANE PROTEIN SCAVE		(FRAGMENT)		CYCLOPHILIN C-ASSOCIAT	EBNERIN.		SPERM-ACTIVATING	HENSIN.	PROTEIN	RECEPTOR	

ALIGNMENTS

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Matches 5
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EMBL: Y14953; CAA75175.1; -.
HSSP: P10998; IVVC.
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Eukarvota; Metazoa; Porifera;
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01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SCAVENGER RECEPTOR CYSTEINE-RICH PROTEIN PRECURSOR.
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
                                                                                                                                                                                                                                 PROSITE; PS00420; SI SEQUENCE 2043 AA;
                                                                                                                                                                                                                                                                                                                                    BLUMBACH B., PANCER Z., DIEHL-SEIFERT B., MUELLER I., MUELLER W.E.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenetics 0:0-0(1999).
EMBL; AF076513; AAD05493.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                        Astrophorida;
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                                                                      GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVICD
                                                                                                                          VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
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da; Geodiidae;
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Pred. No. 4.10e-7;
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Pred. No. 6.99e-76;
18; Mismatches 28;
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SCAVENGER RECEPTOR CYSTEINE-RICH
WW; CBE8C531 CRC32;
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DANGOTT L.J., JORDAN J.E., BELL "Cloning of the mRNA for the properties speract.";

Proc. Natl. Acad. Sci. U.S.A. 8:
EMBL; U30933; AAA75510.1; -.
PFAM; PF00530; SRCR; 4.
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01-NOV-1996
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01-NOV-1996
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01-NOV-1999
                                                                                                                 Signal.
SIGNAL
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MEDLINE: 93300818.
KOTHS K., TAYLOR E., HALENBECK R., CASIPIT C., WANG A.;
"Cloning and characterization of a human Mac-2-binding protein,"
"Cloning and characterization of a human macrophage scavenger re
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DANGOTT L.J., RANKIN T.L.;

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EMBL; X79089; CAA55699.1;
PFAM; PF00530; SRCR; 1.
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J. Biol. Chem.
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Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
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                                                             SEQUENCE
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RESULT 6
1D 077898 PRELIMINARY;
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                                                                                                                                             SEQUENCE
                                                                                                                                                                              Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A new macrophage differentiation antigen scavenger receptor superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE; 93380506.
LAW S.A., MICKLEM K.J.,
MASON D.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
 507
                        774
                                                447
                                                           714 LRLVNGGGRCAGRVEIYHEGSWGTICDDSWDLSDAHVVCRQLGCGEAINATGSAHFGEGT 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507
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                                                                                             Local Similarity
nes 51; Conser
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                                                                                                                                                                                                               Y18395; CAB45233

Y18396; CAB45233

Y18397; CAB45233

Y18398; CAB45233

Y18399; CAB45233

Y18400; CAB45233

Y18401; CAB45233

Y18401; CAB45233

Y18401; CAB45233

Y18403; CAB45233
                                                                                                                                                                                                                                                                                                                         itted (NOV-1998) to t

722968; CAB40541.1;

718388; CAB45233.1;

718389; CAB45233.1;

718390; CAB45233.1;

718391; CAB45233.1;

718392; CAB45233.1;

718393; CAB45233.1;

718394; CAB45233.1;
GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
                      GPIWLDEMKCNGKESRIWQCHSHGWGQQNCRHKEDAGVIC 813
                                            VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
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                                                                                                                                                                                                     PF00530; SRCR;
                                                                                                                                                                                          PR00258; SPERACTRCPTR.
                                                                                                                                                                              Signal.
                                                                                                                                             1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                BUECHLER C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 12,
                                                                                            50.2%;
larity 51.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                40
1116
6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23:2320-2325(1993).
                                                                                                                                          40 POTENTIAL
16 M130 ANTIC
120979 MW; F193FI
                                                                                                                                                                                                                                                                                                                                                                                                                                      O.f.
                                                                                                                                                                                                                                                                                                                                                                                                                       LANGMANN T., SCHMITZ G.; f the human CD163 gene."; the EMBL/GenBank/DDBJ databases
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                                                                                           Score 380; DB 4;
Pred. No. 4.49e-68;
19; Mismatches 30
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Last sequence up
Last annotation
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                                                                                                                                          F193FBBA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
                                                                                                                                                         ANTIGEN
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                                                                                             30;
 546
                                                                                                                    Length 1116;
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Q07901;
Q1-NOV-1996
Q1-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q07899;
Q07899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
M130 ANTIGEN, CYTOPLASMIC VARIANT 1 PRECURSOR.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAW S.A.,
MASON D.Y.
                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                   scavenger receptor superfamily.";
Eur. J. Immunol. 23:2320-2325(1993).
EMBL; Z22969; CAA80542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M130 ANTIGEN, EXTRACHOMO Sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                            SEQUENCE
                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 93380506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 93380506.
                                                                                                                                                                                                       Antigen; Signal
                                                                                                                                                                                                                            PRINTS; PR00258; SPERACTRCPTR.
                                                                                                                                                                                                                                                  PFAM; PF00530;
                                                                                                                                                                                                                                                                                                                                                        MASON D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                scavenger receptor superfamily
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714 LRLVNGGGRCAGRVEIYHEGSWGTICDDSWDLSDAHVVCRQLGCGEAINATGSAHFGEGT 773
                                                                                                                                                                                                                                                                                                                                'A new macrophage differentiation antigen which
                                                                                                                                                                                                                                                                                                                                                                           LAW S.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPIWLDEMKCNGKESRIWQCHSHGWGQQNCRHKEDAGVIC 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
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Z22971; CAA80544.1; -.
                                                   50.2%;
Similarity 51.0%;
51; Conservation
                                                                                                                                                                                                                                                                                                                                                                         MICKLEM K.J.,
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                                                                                                                                          41 11:
1151 AA;
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(TremBLrel. 01, Last sequence update)
(TremBLrel. 12, Last annotation updat
... ¬v¬PACELLULAR VARIANT PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                    SRCR;
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                                                                                                                                          1151 M13
h; 124820 MW;
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                                                                                                                                                                                                                                                                                                                                                                         SHAW J.M., ZHANG X.P., DONG Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHAW J.M.,
                                                   Score 380; DB 4; Leur
Pred. No. 4.49e-68;
Pred. No. 4.49e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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Pred. No. 4.49e-68;
                                                                                                                                          M130 ANTIGEN, CYTOF
                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M130 ANTIGEN, EXTRACELLULAR VARIANT W.; 4901C708 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
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                                                                                                                                                                CYTOPLASMIC VARIANT
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                                                                                                 Length 1151;
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                                                                                                                                                                                                                                                                                                                                  member of the
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VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506

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RESULT 99
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AC 007900;
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DT 01-NOV-
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OC ENKARYC
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RN [1]
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RX MEDLINE
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PANCREAS CANCER-ASCOCIATED PROTEIN 4.
Mesocricetus auratus (Golden hamster).
Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocr
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLRel. 12, Last annotation update)
M130 ANTIGEN, CYTOPLASMIC VARIANT 2 PRECURSOR.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"A new macrophage differentiation antigen
                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00530; SRCR; PRINTS; PR00258; SPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P70117;
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SIGNAL
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MEDLINE; 93380506.
LAW S.A., MICKLEM K.J.,
                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 222970; CAA80543.1; -. PFAM; PF00530; SRCR; 9.
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                                                                                       447
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00420;
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20
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                                                                                                                                                  24
                                                                                                                                                                                                                                   Match 49.4%;
Local Similarity 49.0%;
                                                                                   MRLVNGASANEGRVEIFYRGQWGTVCDNLWNILDANVVCRALGYENATQALGRAAFGPGR 83
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                           GPVMLDEVECTGTEPSLANCSSLGWLKSRCGHEKDAGVVC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                U73375; AAB18745.1;
                                                                                                                                                                                                             49;
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1156 AA;
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1156
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                                                                                                                                                                                                                                                                                                                             64398 MW;
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to the EMBL/GenBank/DDBJ
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56 M130 ANTIGEN, CYTOPLASMIC VARIANT
125352 MW; 287A07A0 CRC32;
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                                                                                                                                                                                                Score 374; DB 11; L
Pred. No. 1.43e-66;
Pred. No. 1.43e-32;
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Pred. No. 4.49e-68;
19; Mismatches 30
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'DDBJ databases
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MEDLINE; 95171455.
ELOMAA O., KANGAS M., S
LIAKKA A., THESLEFF I.,
"Cloning of a novel bac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JLT 11
070513
070513;
01-AUG-1998
01-AUG-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  060754 PRELIMINARY;
060754;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065438; AAC17177.1; -
PROSITE; PS00420; SECRACT_RECEPTOR; 1.
PFAM; PF00530; SRCR; 1.
PRINTS; PR00258; SPERACTRCTTP
                                                                                                                                                                                           PRINTS; PR00258; SEQUENCE 518 A
                                                                                                                                                                                                                     EMBL; U18424; AAA68638.1; -
PFAM; PF01391; Collagen; 4.
PFAM; PF00530; SRCR; 1.
                                                                                                                                                                                                                                                                     scavenger receptors a Cell 80:603-609(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA BINDING MACROPHAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Enkarvota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
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                                                                             423 VRIMGGTNR--GRAEVYYNNEWGTICDDDWDNNDATVFCRMLGY---SRGRALSSYGGGS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 GPIMLDEVECTGNESSLANCSSLGWMVSH-CGHEKDAGVVC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 51.5%; tes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 MRLVNGASASEGRVEIFYRGRWGTVCDNLWNLLDAHVVCRALGYENATQALSRAAFGPGK 83
GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
                                                             VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK:506
                               GNIWLDNVNCRGTENSLWDCSKNSWGNHNCVHNEDAGVEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPIHVDNVKCTGNERSLADCIKQD-IGRHNCRHSEDAGVIC
                                                                                                                        h 48.7%;
Similarity 54.0%;
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        574 AA; 63772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                           AA;
                                                                                                                                                                                           SPERACTRCPTR.
A; 52730 MW;
                                                                                                                                                                                                                                                                                    ., SAHLBERG C., TUUKKANEN J.,
I., KRAAL G., TRYGGVASON K.;
bacteria-binding receptor str
and expressed in a subset of
                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07,
                                                                                                                          Score 369; DB 11;
Pred. No. 2.56e-65;
17; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.54e-66;
18; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                           A2671036 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0FF757E3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                574
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ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
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546
                             517
                                                                                                                                                                                                                                                                                      structurally related of macrophages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546
                                                                                                                                                          Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 574;
                                                                                                                                                                                                                                                                                                                                      SORMUNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                          Gaps
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                                                                                                                            2
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Q60997

PRELIMINARY;

PRT;

2083

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В
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                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U37438; AAC52505.1; - HSSP; P29392; ISFP. MGD; MGI:106210; Crpd. PFAM; PF00431; CUB; 5. PFAM; PF00530; SRCR; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BALB/C; TISS MEDLINE; 96362470. CHENG H., BJERKNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "CRP-ductin: a gene expressed in and hepatic ducts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-NOV-1999 (TrEMBLrel. 12, CRP-DUCTIN PRECURSOR (CRP). CRPD OR CRP OR CRP-DUCTIN.
                                    Q9Y5Y8;

01-NOV-1999 (TrEMBLrel. 12,

01-NOV-1999 (TrEMBLrel. 12,

01-NOV-1999 (TrEMBLrel. 12,

LYSYL OXIDASE-LIKE PROTEIN 2
                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
DOMAIN
DOMAIN
                                                                                                    Q9Y5Y8
                                                                                                                                                                           1568
                                                                                                                                                                                                               1508 LRLVNGSNRCEGRVEILYRGSWGTVCDDSWGISDANVVCRQLGCGSALSAPGNAWFGQGS 1567
                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q60997;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                  447
                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00100;
                                                                                                                                                    597
                                                                                                                                                                                                                                                    Watch 48.7%; Local Similarity 52.0%; nes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IT. Rec. 244:327-343(1996).

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN (CRP-ALPHA AN BETA) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.

SEQUENCE SHOWN HERE IS THAT OF CRP-ALPHA.

TISSUE SPECIFICITY: INTESTINE AND PANCREAS. IN THE COLON,

EXPRESSED IN CRYPT CELLS BUT NOT MATURE VILLUS CELLS. MOST I

EXPRESSED IN MID-CRYPT. ALSO EXPRESSED IN EPITHELIUM LINING

HERATIC AND PANCREATIC DUCTS.
                                                                                                                                                               GLIVLDDVSCSGYESHLWNCHHPGWLVHNCRHSEDAGVIC 1607
                                                                                                                                                 GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546
                                                                                                                                                                                                  VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  '00100; zona_pellucida; 1.
PR00258; SPERACTRCPTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                  29
29
986
1250
1610
2043
                                                                                                                                                                                                                                                                                                     2083
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-JEJUNUM
                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                          2083
2042
1017
1259
1625
2065
2083
                                                                                                                                                                                                                                                                                                     226734
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing
                                        2
                                                                                                                                                                                                                                                                                                    MW;
                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                    Score 369; DB 11;
Pred. No. 2.56e-65;
16; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
  Craniata;
                                                                                                                                                                                                                                                                                                                   CRP-BETA
                                                                                                                                                                                                                                                                                                                           THIDRGQPPSTKL ->
                                                                                                                                                                                                                                                                                                                                        LAVEDVKKPASSQAVYPTAAIFGGVFLAMVLAVAAFTLGRR
                                                                                                                                                                                                                                                                                                                                                                 PRO/SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                           PRO/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                               CRP-DUCTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intestinal crypts and
                                                                                                                                                                                                                                                                                                     945FC070 CRC32;
                                                                                                  638
 Vertebrata;
                                                                                                  A
                                                                                                                                                                                                                                                    32,
                                                                                                                                                                                                                                                                                                                           PELSSQSQGPSSH
                                                                                                                                                                                                                                                                         Length 2083;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus
 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAME GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOST HIGHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreatic
                                                                                                                                                                                                                                                    0;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 48.6%;
Best Local Similarity 51.0%;
Matches 52; Conservative
                                                                                                       Matches
                                                                                                                                                          PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                  OY4K5
OY4K0 PRELIMINARY; PRT; 774 AA.
O9Y4K0;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation updat
LYSYL OXIDASE-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURDAN LE SAUX C., CSISZAR K.;
Submitted (JAN-1999) to the EMBL/GenBa
EMBL; AF117949; AAD34343.1;
PROSITE; PS00420; SPERACT RECEPTOR; 1.
SEQUENCE 638 AA; 71101 MW; C232E6;
                                                                                                                                                                                   J. Biol. Chem. 0:0-0(1997)
EMBL; U89942; AAB49697.1;
                                                                                                                                                                                                                                        SAITO H.,
                                                                                                                                                                                                                                                                               Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                        WS9-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 99
SAUX C.J.,
                                                 447
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-SPLEEN, PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSISZAR K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=SPLEEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The LOXL2
506
                          385
                                                                  326 VRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVSASVVCRELGF-GSAKEAVTGSRLGQG 384
                                                                                                                                                                                                              Regulation of a Novel Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                         506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 VRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVSASVVCRELGF-GSAKEAVTGSRLGQG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem.
                                                 VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPAR-ARTMAYFGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPAR-ARTMAYFGEG
             | IGPIHLNEIQCTGNEKSIIDC-KFNAESQGCNHEEDAGVRCN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVICD
KGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGPIHLNEIQCTGNEKSIIDC-KFNAESQGCNHEEDAGVRCN 224
                                                                                                      Similarity
52; Conser
                                                                                                                                                          PS00420; $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99230328
                                                                                                                                                                                                                                        PAPACONSTANTINOU J., SATO H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene encodes a new lysyl oxidase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRONECKER H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            high levels in reproduct
m. 274:12939-12944(1999).
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLACENTA;
                                                                                                                                                          SPERACT_RECEPTOR; 86724 MW; 1A5C
                                                                                                                  48.6%;
51.0%;
                                                                                                                                                                                                              ene Encoding a
Senescence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOGIC L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                     Score 368; DB 4; Le
Pred. No. 4.54e-65;
21; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 368; DB 4;
Pred. No. 4.54e-65;
21; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reproductive tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C232E6A4 CRC32;
                                                                                                                                                          1A5C47AA CRC32;
                                                                                                                                                                                                                                                                                Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRYANT-GREENWOOD G.D.,
                                                                                                                                                                                                                          Lysyl Oxidase-Related Protein
                                                                                                                                                                                                                                        GOLDSTEIN
                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                               Length 774;
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547
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                                                                                                      Indels
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                                                                                                      ω
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                                                                                                      Gaps
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US-09-147-947-6-06.rsp Art. Mb. 3is available

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ch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 13 10:33:26 2000; MasPar time 6.50 Seconds 464.390 Million cell updates/sec

Tabular output not generated.

Title:

Sequence:

Description: Perfect Score: >US-09-147-947-6 (447-547) from US09147947A.pep (6 of 6) 757

1 VRLMDGENKKEGRVEVFING.....KQDIGRHNCRHSEDAGVICD 101

Scoring table: PAM 150 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Patabase: swiss-prot38 1:swissprot

Statistics: Mean 38.951; Variance 57.048; scale 0.683

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result-being printed, and is derived by analysis of the total score distribution.

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7757 3681 3682 3682 3591 1150 1150 1150 1150 1150 1150 1150 1	Score
100 0 95.6 50.9 447.8 447.8 46.4 46.4 114.9 112.5 111.1 111.1	% Query Match
875 761 453 454 454 458 1436 458 1039 1069 1019 495 495 495 495 495 495 495 495 495 49	Length
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NETR_HUMAN NETR_MOUSE MSRE_BOVIN MSRE_RABIT MSRE_HUMAN SER_STRPU CD6_HUMAN SPER_STRPU CD6_HUMAN ENTK_HUMAN ENTK_HUMAN ENTK_HOWAN CD5_BOVIN CD5_HUMAN CD5_HUMAN CD5_HUMAN CD5_HUMAN CD5_HUMAN CD5_HOUSE BPA1_STRAU CD5_HOUSE SPA1_STRAU VE2_HPV30 9612_LTVCSC XDH_DROSG XDH_DROSG XDH_DROSG	SUMMARIES
NEUROTRYPSIN PRECURSOR NEUROTRYPSIN PRECURSOR NACROPHAGE SCAVENGER R MACROPHAGE SCAVENGER R MACROPHAGE SCAVENGER R ACTIGEN WC1.1. MACROPHAGE SCAVENGER R EGG PEPTIDE SPERACT RE T-CELL DIFFERENTIATION ENTEROPEPTIDASE PRECUR ENTEROPEPTIDASE PRECUR ENTEROPEPTIDASE PRECUR ENTEROPEPTIDASE PRECUR ENTEROPEPTIDASE PRECUR ENTEROPEPTIDASE PRECUR ENTEROPEPTIDASE PRECUR T-CELL SURFACE GLYCOPR T-CELL SURFACE GLYCOPR T-CELL SURFACE GLYCOPR T-CELL SURFACE GLYCOPR T-CELL SURFACE GLYCOPR T-CELL SURFACE GLYCOPR T-CELL SURFACE GLYCOPR T-CELL SURFACE GLYCOPR T-CELL SURFACE GLYCOPR NON-HAEM BROMOPEROXIDA REGULATORY PROTEIN E2. STYLE DEVELOPMENT-SPEC XANTHINE DEHYDROGENASE	Description
7.67e-17. 1.50e-74. 5.00e-74. 5.00e-73. 1.74e-69. 1.27e-67. 5.73e-68. 1.27e-16. 7.38e-57. 1.38e-57. 1.38e-57. 1.38e-90. 2.73e-09.	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	
75	76	76	77	77	77	77	77	77	78	78	79	80	80	80	80	81	81	81	81	81	83	
9.9	10.0	10.0	10.2	10.2	10.2	10.2	10.2	10.2	10.3	10.3	10.4	10.6	10.6	10.6	10.6	10.7	10.7	10.7	10.7	10.7	11.0	
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MYCO_STRCI	METL YEAST	RPC1 BP186	XDH_EMENI	VGL2_IBVM	YHF0_YEAST	CD5_RAT	HMCS_YEAST	YKP9_KLULA	IMD2_MOUSE	NIFH_FRAAL	DAF_CAVPO	ABF2_BACOV	KAP1_RAT	KAP1_MOUSE	KAP1_HUMAN	YJW5_YEAST	YIR7_YEAST	XDH_DROME	MIAA_AQUAE	NIFH_FRASP	P72_HUMAN	
MYCOLYSIN PRECURSOR (E		REPRESSOR PROTEIN CI		E2 GLYCOPROTEIN PRECUR	HYPOTHETICAL 79.0 KD P	T-CELL SURFACE GLYCOPR	HYDROXYMETHYLGLUTARYL-	HYPOTHETICAL KILLER PL	INOSINE-5'-MONOPHOSPHA	NITROGENASE IRON PROTE	COMPLEMENT DECAY-ACCEL	ALPHA-L-ARABINOFURANOS	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	CAMP-DEPENDENT PROTEIN	HYPOTHETICAL 197.6 KD	HYPOTHETICAL 197.5 KD	XANTHINE DEHYDROGENASE	TRNA DELTA(2)-ISOPENTE	NITROGENASE IRON PROTE	PROBABLE RNA-DEPENDENT	
			2.35e+00	2.35e+00	2.35e+00	2.35e+00			1.64e+00	1.64e+00	1.13e+00	7.82e-01	7.82e-01	7.82e-01	7.82e-01	5.38e-01	5.38e-01	5.38e-01		5.38e-01	2.52e-01	

ALIGNMENTS

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387	280	170	93	23	21	1	Serine	PS00420;	PSOUL35;	PSOULS4;	AJUU1531; CA		an email t	requires	and this			he Swiss	SWISS-PROT entry is				TRYPSIN FAMILY.			LEARNING AND MEMORY	ACTION MAY SUBSERVE	ON: PLAYS	iophys.	nd seque	GSCHWEND	8201705.		FROM N.A	ET TIME CES,	Drimator;	ns (Human)				(Re	9 (Rel.			
487	381	271	165	. 92	875	20	protease;	SPERACT_RECEPTOR;	TRYPSIN_SER;	TRYPSIN_HIS;	CAA04816.1;		to license		ä	it institutions	formatics			1	4	CONTAINS 1	:	Ö	LOCATION: SECRETED.		SERVE STR	S A ROLE	Acta 1396	ncing c) T.P., S						_	•	PRECURSOR (EC		Last	39, Created)		STANDARD:	
			KRINGLE.	PROLINE-RICH	NEUROTRYPSIN	POTENTIAL.	Ó	ECEPTOR; 3.	ER; 1.		.'		license@isb-sib.ch).	agreement (See	17			Bioinfo	copyright. It is		SRCR DOMAINS.	KRINGLE DOMAIN		PEPTIDASE FAMILY		YB)	STRUCTURAL REORGE	A ROLE IN NEURONAL PLASTICITY	Biophys. Acta 1396:143-147(1998).	CDNA 6	S@NDEREGGER P.;				Caraillini, Homilinae,	a; crantaca; v			3.4.21) (MOI	annotation update	sequence updat	ed)		PRT: 875	
	,						Kringle;								. Usage	as its	D)	and	produced					[LY S1; ALSO				ASTICITY AND		human					, nono.	riebrata;			(MOTOPSIN).	late)	ie)			AA.	
							Repeat; Signal							w.isb-sib.	by and for		es	the EMBL	hrough a co					KNOWN AS			SOCIA	THE	,	neurotrypsin.						Maiilliatta;									
							nal.							http://www.isb-sib.ch/announce/	ommero	no	ions on its	EMBL outstation -	through a collaboration					THE			WITH	PROTEOLYTIC		n. ";															

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                                             modified
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Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                                                                     nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
NEUROTRYPSIN PRECURSOR (EC 3.4.21.-) (MOTOPSIN)
PROTEASE 3) (BSSP-3).
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DOMAIN
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GSCHWEND T.P., KRUEGER
                                                                                                                                                                                                                                                                               MEDLINE; 98008848.
YAMAMURA Y., YAMASHIRO K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447
                                                                                                                                                                                                                                                         "Molecular cloning
                                                                                                                                                                                                                                                                     YAMAGUCHI N.;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         "Neurotrypsin, a novel
hervous system.";
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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(aryota; Metazoa; Chordata; Craniata; Ver
(aryota; Metazoa; Chordata; Craniata; Ver
                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation. European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffied and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                            FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH LEARNING AND MEMORY OPERATIONS.
TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL CORTEX, HIPPOCAMPUS
                                                                                                            SIMILARITY: CONTAINS SIMILARITY: CONTAINS
                                                                                                                                             SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO
                                                                                                                                 TRYPSIN FAMILY.
                                                                                                                                                                    AND AMYGDALA
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                      license@isb-sib.ch)
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POTENTIAL.
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REACTIVE BOND (POTENTIAL).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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'.67e-177;
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ae; Murinae;
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Matches 9
                                                       KUHRER L., FREEMAN M., KODAMA ! "Coiled-coil fibrous domains me scavenger receptor type II."; Nature 343:570-572(1990).
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DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSRE_BOVIN STANDARD; PRT; 453 AA. P21758; 01-MAY-1991 (Rel. 18, Created) 01-MAY-1991 (Rel. 18, Last sequence update) 01-FEB-1994 (Rel. 28, Last annotation update) MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II LDL RECEPTOR I AND II
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CARBOHYD
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Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Cetartiodactyla; Ruminantia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
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DOMAIN
                                                                                                                                                                                                                               "Type I macrophage scavenger collagen-like coiled coils." Nature 343:531-535(1990).
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PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; PS00420; SPERACT_RECEPTOR;

PROSITE; PS00420; SPERACT_RECEPTOR;

PROSITE; PS00420; SPERACT_RECEPTOR;
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          KRIEGER M.;
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                                                                                                                                                                                                                                                                                                                                                 TISSUE=LUNG;
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EMBL; D89871; BAA23986.1;
MGD; MGI:1100881; PRSS12.
PFAM; PF00530; SRCR; 3.
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 FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PAT
DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ART
TWO TYPES OF RECEPTOR SUBMNITS EXIST. THESE RECEPTORS
ENDOCYTOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCL
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92.1%;
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POTENTIAL.
1; 3F3C4F35
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                                                                                                                mediate
                                                                                                                                                                                                                                                                    receptor contains alpha-helical and
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KRINGLE.
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                                                                                                                PENMAN M.,
ate ligand b
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                                                                                                                                                                                                                                                                                                                                                                                                                          Pecora;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC32;
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                                                                                                                                                                                                                                                                                                            MATSUDAIRA
                                                                                                                                                                                                                                                                                                                                                                                                                          Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
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               E PATHOLOGIC
G ATHEROGENESIS.
G ATHEROGENESIS.
                                                                                                                macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae,
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Best Local
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EMBL; X54183; CAA38108.1; -.
PIR; S08276; S08276
PIR; S08278; S08278
PROSITE; PS00420; SPERACT_RECEPTOR; 1.
PFAM; PF00530; SRCR; 1.
PFAM; PF01391; Collagen; 1.
Transmembrane; Glycoprotein; Endocytosis
                                                                                                                                                                                                                                          005585;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II (MACROPHAGE ACETYLATED
MEDLINE; 93016877.

MEDLINE; 93016877.

BICKEL P.E., FREEMAN M.W.;

"Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells express" inducible macrophage "Rabbit aortic smooth muscle cells exp
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the European Bioinformatics Institute. The
use by non-profit institutions as long
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entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                             Oryctolagus
                                                                                                                                                                                                                                                                                                                                                           MSRE_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through
                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MODIFIED LOW DENSITY LIPOPROTEINS (LDL).
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF THE SAME GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR (TYPES I AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPIWLNEVFCFGKESSIEECRIRQWGVRACSHDEDAGVTC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                            GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 50; Conse
                                                                                                                                                     Lagomorpha;
                                                                                                                                                                    cuniculus (Rabbit).
Metazoa; Chordata; Craniata; Vertebrata; Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.9%;
                                                                                                                                                   Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor: Alternative splicing.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
SPACER (PROBABLE).
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17; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 385; DB 1; Pred. No. 5.00e-74;
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QS -> PG (IN ISOFORM II).
MISSING (IN ISOFORM II).
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TWO FORMS OF MACROPHAGE SCAVENGER
ARE PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2CDE1EE1 CRC32;
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                                                                                                                                                   Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                           454
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                                                                                                                                                                                                                                                                                                                                                           A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 453
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Best Local S
Matches 4
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SEQUENCE FROM N.A.
MEDLINE; 93131972.
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CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                           DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol.
                                                                                                                                                                       VARSPLIC CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                     Heptad repeat pattern; Receptor; Alternative splicing.

DOMAIN 1 50 CYTOPLASMIC (POTENTIAL).

TRANSMEM 51 73 SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00530; SRCR; 1.
PFAM; PF01391; Collagen; 1.
Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L11693; AAA31402.1; ...
EMBL; L11692; AAA31403.1; ...
EMBL; D13381; BAA02649.1; ...
PROSITE; PS00420; SPERACT_RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              charged macromolecules by macrophage scavenger receptors.";
J. Biol. Chem. 268:2126-2133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOI T., WADA Y., KODAMA T., HIGASHI
MIYAZAKI T., NAKAMURA H., UESUGI S.,
ITAKURA H., YAZAKI Y., MATSUMOTO A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Clin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells.";
507
                          413
                                                    447
                                                                             353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charged collagen structure mediates the recognition of negatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THE TWO FORMS OF MACROPHAGE SCAVENGER
RECEPTOR (TYPES I AND II) ARE PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3iol. Chem. 268:2126-2133(1993).

FUNCTION: MEMBRANE GLYGOPROTEINS IMPLICATED DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF THE SAME GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTED OF MACROMOLECULES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MODIFIED LOW DENSITY LIPOPROTEINS (LDL)
                                                                            VRLVGGRGPHEGRVEILHNGQWGTVCDDHWELRAGQVVCRSLGYRGVKSVHKKAYFGQGT 412
GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
                        GPIWLNEVPCLGMESSIEECKIRQWGVRVCSHGEDAGVTC 452
                                                   VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                                                                       Similarity
49; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long
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                                                                                                                                                                                                            102
143
184
221
249
267
                                                                                                                                                           ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                                           454
109
272
344
454
82
                                                                                                                  50.3%;
                                                                                                                                                           49745
                                                                                                                                                            MΨ,
                                                                                                     Score 381; DB 1; Le
Pred. No. 5.89e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIGASHI K.I., KURIHARA
ESUGI S., IMANISHI T., K
                                                                                                                                                         TPSATVR -> RPVQLTP ()
MISSING (IN ISOFORM)
H -> D (IN REF. 2).
July 5D780348 CRC32;
                                                                                                                                                                                                                          POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                  SPACER (PROBABLE).
ALPHA-HELICAL COILED-COIL
                                                                                                                                                                                                                                                                                                                                                                                                                              Endocytosis; Coiled coil;
                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                        CYS-RICH
                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                 RPVQLTP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T., KAWABE Y.,
                                                                                                                               Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN THE PATHOLOGIC DURING ATHEROGENESIS. RECEPTORS MEDIATE THE
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Λ̈́q
                                                                                                                                                                                                                                                                                                                                                                                                                               LDL;
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                                                                                                      Gaps
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RESULT

MSRE_MOUSE

PRT;

A

RRT RAX

PFAM; PF01391; Collagen; 1

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EMBL; L04274; AAA39747.1; A
EMBL; L04275; AAA39748.1; A
EMBL; D13382; BAA26750.1; T
EMBL; M59445; AAA37464.1; T
EMBL; M59446; AAA37465.1; T
EMBL; U13873; AAC13774.1; T
                                                                                                                                                                                                                                                                                                                                                                                                                  the Euro
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata;
Eukaryota; Rodentia; Sciurognathi; Murida
                                                                                                                                                                                                                                                                                              This
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MEDLINE: 93131972.
DOI T., WADA Y., KODAMA T., HIGASHI K
MIYAZAKI T., NAKAMURA H., UESUGI S.,
ITAKURA H., YAZAKI Y., MATSUMOTO A.;
"Charged collagen structure mediates"
 PIR; A38260; A38260.
MGD; MGI:98257; SCVR.
PROSITE; PS00420; SPE
                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FREEMAN M., ASHKENAS J., REES JENKINS N.A., KRIEGER M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 349-458 FROM N.A. MEDLINE; 91062370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               charged macromolecules by macrophage scavenger receptors.",
J. Biol. Chem. 268:2126-2133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structures and high and low affinity murine type I and type II macrophage J. Lipid Res. 34:983-1000(1993).
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MSR1 OR SCVR.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
MACROPHAGE SCAVENGER RECEPTOR TYPES I AND II (MACROPHAGE ACETYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P30204;
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFTRING R.P., FREEMAN M.W.;
"Structure of the murine macrophage scavenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: THE TWO FORMS OF MACROPHAGE SCAVENGER RECEPTOR (TYPES I AND II) ARE PRODUCED BY ALTERNATIVE SPLIC
                                                                                                                                                                                                                                                          European Bioinformatics Institute.
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93359822.
J., PENMAN
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                                                                                         AAA39747.1; ALT_INIT.
AAA39748.1; ALT_INIT.
BAA02650.1; -.
AAA37464.1; -.
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AMURA H., UESUGI S., IMANISHI T., KAWI
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SPERACT_RECEPTOR;
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II murine macrophage scavenger
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MENIATE THE
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P30205;
01-APR-1993
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SEQUENCE
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or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                             modified and this statement
                                                                                                                                                                                                                                                                                                                                                          "Molecular characterization of the WC1 antigen on bovine CD4-CD8-gamma delta T lymphocytes."; J. Immunol. 149:3273-3277(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota; Metazoa;
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CYTOPLASMIC (POTENTIAL).
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   362; DB 1;
No. 6.88e-68;
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No. 1.74e-69;
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                     DB 1;
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                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the Buropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSRE_HUMAN STANDARD; PRT; 451 AA. P21757; P21759; 01-MAY-1991 (Rel. 18, Created) 01-MAY-1991 (Rel. 18, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) MACROPHAGE SCAVENCER RECEPTOR TYPES I AND II
                                                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human macrophage scavenger receptors: primary structure, expression, and localization in atherosclerotic lesions.";
Proc. Natl. Acad. Sci. U.S.A. 87:9133-9137(1990).
-i- FUNCTION: MEMBRANE GLYCOPROTEINS IMPLICATED IN THE PATHOLOGIC DEPOSITION OF CHOLESTEROL IN ARTERIAL WALLS DURING ATHEROGENESIS.
TWO TYPES OF RECEPTOR SUBUNITS EXIST. THESE RECEPTORS MEDIATE THE DEDOCTYPOSIS OF A DIVERSE GROUP OF MACROMOLECULES, INCLUDING
                                                                                                                                                                              PFAM; PF00530; SRCR; 1.
PFAM; PF01391; Collagen; 1.
Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                       EMBL; D90187; BAA14208.1; -.
EMBL; D90188; BAA14209.1; -.
PIR; A38415; A38415.
B38415; B38415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATSUMOTO A., NAITO M., ITAKURA H., IKEMOTO S., ASAOKA H
HAYAKAWA I., KANAMORI H., ABURATANI H., TAKAKU F., SUZUK
KOBARI Y., MIYAI T., TAKAHASHI K., COHEN E.H., WYDRO R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata;
                                             CARBOHYD
                                                             DOMAIN
                                                                                                        DOMAIN
                                                                                                                                      TRANSMEM
                                                                                                                                                     DOMAIN
                                                                                                                                                                   Heptad repeat
                                                                                                                                                                                                                            PROSITE; PS00420; SPERACT_RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HOUSMAN D.E., KODAMA T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDL RECEPTOR I AND II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN ALTERNATIVE PRODUCTS: THE TWO FORMS OF MACROPHIA RECEPTOR (TYPES I AND II) ARE PRODUCED BY ALTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MODIFIED LOW DENSITY LIPOPROTEINS (LDL). SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF THE SAME GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPIWLDNLNCTGKESHVWRCPSRGWGQHNCRHKQDAGVIC 475
                                                                                                                                                                                                                                            153622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
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                                                                                                      t pattern;
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51 76
77 451
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                                                                                                                   Receptor: Alternative splicing.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANGOR (TYPE-II MEM
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                              Endocytosis; Coiled coil;
                                                                        ALPHA-HELICAL COILED-COIL COLLAGEN-LIKE.
               POTENTIAL.
                                                             CYS-RICH
                                                                                                   SPACER (PROBABLE)
                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MACROPHAGE SCAVENGER
BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
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                                                                                                                                  MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                           restrictions
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  Query Match
Best Local Similarity
Matches 53; Conser
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Best Local
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SEQUENCE
                                                                                                                                                                                                  DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                             Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPER_STRPU
P16264;
                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DANGOTT L.J., JORDAN J.E., "Cloning of the mRNA for t peptide speract."; Proc. Natl. Acad. Sci. U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
EGG PEPTIDE SPERACT RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00420; SPERA
PFAM; PF00530; SRCR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the s
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DANGOTT L.J., JORD
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                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J04518; AAA30078.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: RECEPTOR FOR THE EGG PEPTIDE SPERACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 477-489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507
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Similarity 49.08;
49; Conservet
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46.4%;
larity 51.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       SPERACT_RECEPTOR; 4.
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17; M
                    Score 351; DB 1;
Pred. No. 5.73e-65;
                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 361; DB 1;
Pred. No. 1.27e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELLET R.A., GARBERS D.L.: protein that crosslinks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN ISOFORM II)
                                                                                                                        POTENTIAL.
                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM II).
                                                                                                                                                                                                                                                                                                                        EGG PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86:2128-2132(1989).
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                                                                                                                                                                                                                                        YTOPLASMIC (POTENTIAL).
X APPROXIMATE TANDEM REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                Signal; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions on ng as its content is in no
                                                                                  CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą
                                                                                                                                                                                                                                                                                                                        SPERACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
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                                       Length 532;
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                                                                                                         Query Match
                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Eutheria; Primates;
[1]
SEQUENCE FROM N.A.
MEDLINE; 92013796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD6_HUMAN
P30203;
01-APR-1993
01-APR-1993
15-DEC-1998
                                                                                                                                              CARBOHYD
CARBOHYD
                                                                                                                                                                      CARBOHYD
CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The lymphocyte glycoprotein CD6 contains a repeated domain characteristic of a new family of cell surface and secreted proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                      PFAM; PF00530; SRCR; 3.
Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-CELL DIFFERENTIATION ANTIGEN CD6
                                    447
            221
                                                                                                                                                                                                                                                                                    HAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÷
                                                                                                                                                                                                                                                           RANSMEM
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                                                                                                                                                                                                                                                                        OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264
                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exp. Med. 174:949-952(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: INVOLVED IN CELL ADHESION. BINDS TO CD16 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: CONTAINS 3 SRCR DOMAINS.

DATABASE: NAME-PROW: NOTE-CD guide CD6 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd6.htm".
                                                                                                                                                                                                                                                                                                                                              $26741; $26741.
186720; -.
           GPIHRDQVNCSGAEAYLWDCPGLP-GQHYCGHKEDAGVVC 259
                                  VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTMAYFGEGK 506
                                                          LRLVDGGGACAGRVEMLEHGEWGSVCDDTWDLEDAHVVCRQLGCGWAVQALPGLHFTPGR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKGPIHVDNVKCTGNERSLADCIKQDIGR-HNCRHSEDAGVIC 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWAPIHTSFVMCTGVEDRLIDCILRD-GWTHSCYHVEDASVVC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRLMDGSGPHEGRVEIWHDDAWGTICDDGWDWADANVVCRQAGYRGAVKASGFKGEDFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARART-MAY-FGE
                                                                                                                                                                                                                                                                                                                                                                    X60992; CAA43306.1;
                                                                                   Similarity 48.0% 48; Conservative
                                                                                                                                                                                                                                                                                                                                PS00420; SPERACT_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa;
                                                                                                                                368
468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                                                                                                      403
424
49
112
112
118
229
339
                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                              468
28
49
112
118
118
339
345
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                                                                                                                                 49828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                  MW;
                                                                                  Score 323; DB 1;
Pred. No. 1.38e-57;
16; Mismatches 35
                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                              CYTOPLASMIC
                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                  T-CELL DIFFERENTIATION ANTIGEN CD6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                  042D5AC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468
                                                                                                                                  CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                       Repeat; Signal
                                                                                   35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (T12) (TP120).
                                                                                                        Length 468
                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
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                                                                                  1;
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                                                                                  Gaps
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RA MIKI K., KUUOKAWA K., TASHIRO K., SHIOKAWA K., SHINOMIYA K.,

RA UMEYAWA H., INOUE H., TAKAHASHI T., TAKAHASHI K.;

RT "Structural characterization of porcine enteropeptidase.";

RL J. BAOL Chem. 269:19976-19982(1994).

CC -!- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC

CC PROTEOLYTIC PROENZYMES (TRYESIN, CYMOTRYPSIN AND CARBOXYPEPTIDASE

CA, IT CATALYZES THE CONVERSION OF TRYESINGEN TO TRYPSIN WHICH IN

CC TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSIN WHICH IN

CC PROCARBOXYPEPTIDASES, AND PROELASTASES.

C. -- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-Lvc-1-**"

C. -- SURHUNTM. ....
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                                       PFOME PFO0629; MAM; 1.

PFAM; PFO0390; SEA; 1.

Signal-anchor; Glycoprotein; M
Serine protease; Zymoden. ...

CHAIN

CHAIN
                                                                                                                     PROSITE: PS50060; MAM_2: 1.
PROSITE: PS501209; LDLRA_1;
PROSITE: PS50068; LDLRA_2;
PFAM; PF00057; ldl_recept_a;
PFAM; PF00057; ltl_recept_a;
PFAM; PF000431; CUB; 2.
PFAM; PF00431; CUB; 2.
PFAM; PF00530; SRCR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENTK_PIG
P98074;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT I CLEAVED BY A TRYPSIN-LIKE PROTEASE.
-!- PTM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.
-!- SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.
-!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
-!- SIMILARITY: CONTAINS 1 SRCR DOMAIN.
-!- SIMILARITY: CONTAINS 1 SRCR DOMAIN.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
                               CHAIN
                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                          EMBL; D30799; BAA
HSSP; P00763; 1DP
PROSITE; PS00134;
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HETEROTRIMER OF A CATALYTIC (LIGHT) CHAIN, A MULTIDOMAIN (HEAVY) CHAIN, AND A MINI CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENTEROPEPTIDASE PRECURSOR (EC 3.4.21.9) (ENTEROKINASE) PRSS7 OR ENTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION:
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 protease;
52
118
800
4EM 19
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PS00740;
PS50060;
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Setartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                         BAA06459.1; -.
                                                                                                                                                                  ld1_recept_a;
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 Zymogen;
117
799
1034
47
                                                                                                                                                                               ; CUB; 2.
; MAM_1; 1.
; MAM_2; 1.
; LDLRA_1; 2.
; LDLRA_2; 2.
                                                                                                                                                                                                                                                          TRYPSIN_HIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33, Created)
33, Last sequence update)
36, Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE II MEMBRANE
                                                             Transmembrane;
NON-CATALYTIC M CHAIN (MINI CHAIN).
NON-CATALYTIC H CHAIN (HEAVY CHAIN).
CATALYTIC L CHAIN (LIGHT CHAIN).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                         Myristate; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                             Repeat.
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                                                                                                                                                                                                                                                                                                                                                   http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN
                                                                                                                                                                                                                                                                                                                                                                   Usage
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st Local s
tches
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CFAI_HUMAN
P05156;
13-AUG-1987
13-AUG-1987
01-OCT-1996
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ACT_SI
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DOMAIN
                         SEQUENCE FROM N.A. TISSUE=LIVER;
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    MEDLINE; 87241401
                                                                                             Eutheria;
                                                                                                              Eukaryota;
                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                    COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447
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                                                                                                                                                                                                                                                                                                                                                                                                                                GPF 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
20; Conser
                                                                                        Primates;
                                                                                                                                                                             7 (Rel. 05, Created)
7 (Rel. 05, Last sequence up
5 (Rel. 34, Last annotation
FACTOR I PRECURSOR (EC 3.4.)
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llarity 31.7%;
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2.57e-16;
ches 23;
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-: FUNCTION: FACTOR I IS RESPONSIBLE FOR CLEAVING THE ALPHA-CHAINS OF C48 AND C3B IN THE PRESENCE OF THE COFACTORS C4-BINDING PROTEIN AND FACTOR H RESPECTIVELY.

-: SUBJUNIT: HETERODIMER OF A LIGHT AND HEAVY CHAINS LINKED BY DISULFIDE BONDS.

-: SUBJULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                 DISULFID DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. [2]
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HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y00318; CAA68416.1; ALT_INIT.
EMBL; J02770; AAA52455.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; pS00134; TRYPSIN_HIS; 1; pS00135; TRYPSIN_SER; 1; pS01209; LDLRA_1; 1.; pS50068; LDLRA_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathway;
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  19.3%;
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COMPLEMENT FACTOR I HEAVY CI
COMPLEMENT FACTOR I LIGHT CI
COMPLEMENT FACTOR I LIGHT CI
LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

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FFAM; PF00530; SRCR; 1.

FFAM; PF00530; SRCR; 1.

PFAM; PF001390; SEA; 1.

PFAM; PF01390; SEA; 1.

PFAM; PF01390; SEA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long hodified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6; TISSUE-DUODENUM;
YUAN X., LU D., RUBIN D.C., PUNG C.Y.M., SADLER J.E.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC
PROTEOLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE
A). IT CATALYZES THE CONVERSION OF TRYPSINGEN TO TRYPSIN WHICH IN
TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINGEN,
PROCARBOXYPEPTIDASES, AND PROELASTASES (BY SINILARITY).

-!- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
ENIEROPEPTIDASE (EC 3.4.21.9) (ENTEROKINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U73378; AAB37317.1; HSSP; P00763; 1DPO.
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PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT
CLEAVED BY A TRYPSIN LIKE PROTEASE (BY SIMILARITY).
SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 1 SRCR DOMAIN.
SIMILARITY: CONTAINS 1 SRCR DOMAIN.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS
THYPEIN TAMELY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HETERODIMER OF A CATALYTIC MULTIDOMAIN (HEAVY) CHAIN LINKED BY
                                                                                                                                                                                                                                                                                                                                                              MGI:1197523; PRSS7.
LITE; PS00134; TRYPSIN_HIS;
LITE; PS00135; TRYPSIN_SER;
LITE; PS001180; CUB; 2.
LITE; PS00740; MAM_1; 1.
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                                                                                                                                                                                                                                                                                                               PS50060;
PS01209;
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; MAM_2; 1.
; LDLRA_1; 2.
; LDLRA_2; 2.
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Best Local :
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01-FEB-1996 (Rel. 3
15-FEC-1999 (Rel. 3
FEMTEROPEPTIDASE PREPRESST OR ENTK.
TISSUE=DUODENUM;
MEDLINE; 94329561.
KITAMOTO Y., YUAN
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Eukaryota; Metazoa; Chordata;
Eutheria; Cetartiodactyla; Rur
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                                              N.A.,
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29.9%;
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NON-CATALYTIC CHAIN (HEAVY CHAIN).

CATALYTIC CHAIN (LIGHT CHAIN).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

LDL-RECEPTOR CLASS A 1.
                                                                                             ta; Craniata; Vertebrata; Mammalia;
Ruminantia; Pecora; Bovoidea; Bovi
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Pred. No. 1.15e-11;
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   MCCOURT D.W.,
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CHARGE RELAY SYSTEM
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                                                  SEQUENCE
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   SADLER J.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1069;
                                                                                               Bovoidea; Bovidae;
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PROSITE; PS00134; TRYPSIN_HIS; 1
PROSITE; PS00135; TRYPSIN_SER; 1
PROSITE; PS00180; CUB; 2.

PROSITE; PS01180; CUB; 2.

PROSITE; PS00740; MAM_1; 1.

PROSITE; PS00799; LDLRA_1; 2.

PROSITE; PS00799; LDLRA_2; 2.

PROSITE; PS01068; LDLRA_2; 2.

PROSITE; PS01068; LDLRA_2; 2.

PROSITE; PS01068; LDLRA_2; 2.

PROSITE; PS01068; LDLRA_2; 2.

PFAM; PF00079; Idl. recept_a; 2.

PFAM; PF00089; LTYPSin; 1.

PFAM; PF00089; CTYPSin; 1.

PFAM; PF00089; SEA; 1.

PFAM; PF00639; MAM; 1.

PFAM; PF01390; SEA; 1.

PFAM; PF01390; SEA; 1.
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EMBL; L19663; AAA1603
PIR; A61436; A61436.
HSSP; P00763; 1DPO.
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-i. FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC PROTEOLYTIC PROENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE A). IT CATALYZES THE CONVERSION OF TRYPSINOGEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINOGEN, PROCARBOXYPEPTIDASES, AND PROELASTASES.

-i. CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN TRYPSINOGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license service.
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MEDLINE; 92189715.
LIGHT A., JANSKA H.;
The amino-terminal sequence of the catalytic subunit of enterokinase.";
                                                   DOMAIN
DOMAIN
                                                                                                                         CHAIN
CHAIN
                                                                                                                                                                          Signal-anchor;
Serine proteas:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
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                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94043122
LAVALLIE E.R., REI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: HETERODIMER OF A CATALYTIC (LIGHT) CHAIN AND A MULTIDOMAIN (HEAVY) CHAIN LIMKED BY A DISULFIDE BOND.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (PROBABLE).
TISSUE SPECIFICITY: INTESTINAL BRUSH BORDER.
PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS CLEAVED BY A TRYPSIN-LIKE PROTEASE.
SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
SIMILARITY: CONTAINS 1 MAM DOMAIN.
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KITAMOTO Y., VEILE R.A., DONIS-KELLER H., SI "CDNA sequence and chromosomal localization the proteolytic activator of trypsinogen."; Biochemistry 34:4562-4568(1995).
                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa;
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"Enterokinase, the initiator of intestinal digestion, is a mosaic protease composed of a distinctive assortment of domains.";

PICC. Natl. Acad. Sci. U.S.A. 91:7588-7592(1994).

-1- FUNCTION: RESPONSIBLE FOR INITIATING ACTIVATION OF PANCREATIC PROTECTIVIC PROCENZYMES (TRYPSIN, CHYMOTRYPSIN AND CARBOXYPEPTIDASE A). IT CATALYZES THE CONVERSION OF TRYPSIN GEN TO TRYPSIN WHICH IN TURN ACTIVATES OTHER PROENZYMES INCLUDING CHYMOTRYPSINGEN, PROCARBOXYPEPTIDASES, AND PROELASTASES.

-1- CATALYTIC ACTIVITY: SELECTIVE CLEAVAGE OF 6-LYS-|-ILE-7 BOND IN
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Serine protease;
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HSSP; P00763;
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KITAMOTO Y., YUAN X.,
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DISEASE: DEFECTS IN PRSS7 CAUSE LIFE-THREATENING INTESTINAL DISEASE: DEFECTS IN PRSS7 CAUSE LIFE-THREATENING INTESTINAL MALABSORPTION CHARACTERIZED BY DIARRHEA AND FAILURE TO THRIV SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS.

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                                                                                                                                                                                                                                                                                                                                                                                Zymogen;
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MAM_2; 1.
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LDLRA_2; 2.
                                                                                                                                                                                          1019
47
223
334
504
634
679
771
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                                                                                                                                                                                                                                                   Transmembrane; Repeat.

NON-CATALYTIC CHAIN (HEAVY CHAIN).
CATALYTIC CHAIN (LIGHT CHAIN).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
LDL-RECEPTOR CLASS A 1.
CUB.
MAM.
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CHARGE
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CHARGE RELAY SYSTEM
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                                                                                                                                                                                                             LDL-RECEPTOR
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Best Local S
Matches 2
   entities
or send a
                                                                                        MEDLINE; 90384847.

YU Q. REICHERT M., BROUSSEAU T., CLEUTER Y., BURN YU Q., REICHERT M., BROUSSEAU T., CLEUTER Y., BURN "Sequence of bovine CD5";

Nucleic Acids Res. 18:5296-5296(1990).

-!- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING PROLIFERATION. CD5 INTERACTS WITH CD72/LYB-2.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- SUBCELLULAR LOCATION: SRCR DOWAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
SEQUENCE
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DISULFID
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PRT; 495 AA.

P15_BOVIN STANDARD; PRT; 495 AA.

P19238;

01-NOV-1990 (Rel. 16, Created)

01-NOV-1990 (Rel. 16, Last sequence update)

01-NOV-1997 (Rel. 35, Last annotation update)

T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR (LYMPHOCYTE GLYCOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                        T1/LEU-1) (LYMPHOCYTE ANTIGEN CD5).
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                                                                                                                                                                                                                              Cetartiodactyla;
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Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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25.5%;
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Pred. No. 2.73e-08;
23; Mismatches 43
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PR PIR; S11270; S11270.

PIR; S11270; S1270.

PEAM; PF00530; SRCR; 3.

W Signal; Transmembrane; Glycoprotein; T-cell.

T SIGNAL

T CHAIN

25 495

T -CELL SURFACE GLYCOPROTEIN CD5.

DOMAIN

25 372

POTENTIAL.

T DOMAIN

403 495

CYTOPLASMIC (POTENTIAL).

TOMAIN

33 134

T DOMAIN

33 134

CARBOHYD

51 51

CARBOHYD

117 CARBOHYD

117 CARBOHYD

118 CARBOHYD

CARBOHYD

369 369

SEQUENCE

495 AA; 54333 MW; F8ED2AEO CRC32;
                                                                                                          Query Match 14.9%;
Best Local Similarity 45.5%;
Matches 20; Conservative
                                                  Score 113; DB 1; Length 495;
Pred. No. 7.16e-07;
8; Mismatches 12; Indels
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